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Compugen Ltd
version - 2004 (
GenCore
(c) 1993
        Copyright
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model **₹** using protein search, OM protein

econds 2004, 14:21:47 30, December Run on:

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US-10-046-922-3 72

CGYWLTIWGC 10 score: Title: Perfect sc Sequence:

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2002273 seqs, 358729299 residues Searched:

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444336 of hits satisfying chosen parameters: Total number

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Database

Geneseq_23Sep04:*
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SUMMARIES

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ALIGNMENTS

Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3; angiogenesis; lymphangiogenesis; vascular endothelial growth factor; cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic; vulnerary; cell surface receptor; cancer; neovascularisation; liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma; diabetes; PDGF; platelet derived growth factor. ID NO:35 standard; peptide; 10 VEGFR-3 binding peptide SEQ entry) (first WO200257299-A2 Homo sapiens Synthetic. 09-JAN-2003 3932 ABP53932 ABP53932; RESULT 1 ABP53932

2002WO-IB000099 16-JAN-2002;

25-JUL-2002

2001US-0262476P 17-JAN-2001;

CANCER RES LICENTIA LTD. (LUDW-) LUDWIG INST (LICN) LICENTIA LTI

Kubo H; 回 Koivunen Alitalo K,

WPI; 2002-691521/74.

New isolated peptide that inhibits VEGF-C and VEGF-D, useful for diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity such as cancer and diseases of neovascularization.

Claim 13; Page 80; 149pp; English.

The present invention describes an isolated peptide (I) that binds to and inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I) have cytostatic, hepatotropic, antiinflammatory, hypotensive, antidiabetic and vulnerary activities, and can be used in gene therapy. Compositions and methods from the present invention are useful for diagnosing, evaluating and treating disorders mediated by the activity of the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,

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liver, spleen, kidney, lymph node, small intestine, blood cells, pancreas, colon, stomach, breast, endometrium, prostate, testicle, ov skin, head and neck, oesophagus, bone, marrow or blood, and diseases neovascularisation, e.g. liver diseases, hypertension, post-trauma, chronic hepatitis, haemangiomas and diabetes. The present sequence represents a specifically claimed VEGFR-3 binding peptide from the
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                                                                                                                                                                                                                                                                                                                                                                                                                           Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3; angiogenesis; lymphangiogenesis; vascular endothelial growth factor; cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic; vulnerary; cell surface receptor; cancer; neovascularisation; vulner disease; hypertension; post-trauma; chronic hepatitis; haemangio diabetes; PDGF; platelet derived growth factor.
liver, spleen, kidney, lymph node, small intestine, blood cells, pancreas, colon, stomach, breast, endometrium, prostate, testicle, ov skin, head and neck, oesophagus, bone, marrow or blood, and diseases neovascularisation, e.g. liver diseases, hypertension, post-trauma, chronic hepatitis, haemangiomas and diabetes. The present sequence represents a specifically claimed VEGFR-3 binding peptide from the
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The invention comprises a method (BRASIL - Biopanning and Rapid Analysis of Selective Interactive Ligands) to obtain a targeting peptide. The BRASIL method of the invention involves: exposing a target to a phage gisplay library in a first phase; exposing the first phase to a second phase; and separating the phage bound to the target from unbound phage.

The BRASIL method of the invention allows cell phages to be separated from the remaining unbound phage in a single differential centrifugation step. When compared to conventional cell panning methods, the BRASIL method shows a significant increase in recovery of specific phage and a substantial decrease in background. The BRASIL method is useful for identifying targeting peptides. The targeting peptides identified by the method of the invention are useful for treating disease states, such as: disease; bacterial infection; viral infection; cardiovascular disease and
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liver, spleen, kidney, lymph node, small intestine, blood cell pancreas, colon, stomach, breast, endometrium, prostate, testi skin, head and neck, oesophagus, bone, marrow or blood, and di neovascularisation, e.g. liver diseases, hypertension, post-tr chronic hepatitis, haemangiomas and diabetes. The present sequi represents a VEGFR-3 binding peptide, which is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BRASIL; targeting peptide; bacterial infection; Biopanning and Rapid Analysis of Selective Interactive Ligands inflammatory arthritis; atherosclerosis; cancer; autoimmune diviral infection; cardiovascular disease; degenerative disease.
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The invention comprises a method (BRASIL - Biopanning and Rapid Analysis of Selective Interactive Ligands) to obtain a targeting peptide. The BRASIL method of the invention involves: exposing a target to a phage of its phase; exposing the first phase to a second phase; and separating the phage bound to the target from unbound phage. The phase in a single differential centrifugation the remaining unbound phage in a single differential centrifugation step. When compared to conventional cell panning methods, the BRASIL method shows a significant increase in recovery of specific phage and substantial decrease in background. The BRASIL method is useful for identifying targeting peptides. The targeting peptides identified by the method of the invention are useful for treating disease states, such as: diabetes; inflammatory arthritis; atherosclerosis; cancer; autoimmune disease; bacterial infection; viral infection; cardlovascular disease and degenerative disease. The invention
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Biopanning and Rapid Analysis of Selective Interactive Ligands; diabinflammatory arthritis; atherosclerosis; cancer; autoimmune disease; viral infection; cardiovascular disease; degenerative disease.
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Pred. No. 1.7e+06;
 DB 5;
                                                                                                                                                                                                                                                 targeting peptide 50.
Score 39.5; D
Pred. No. 1.7e
1; Mismatches
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The BRASIL method of the invention allows cell phages to be separated from the remaining unbound phage in a single differential centrifugation step. When compared to conventional cell panning methods, the BRASIL method shows a significant increase in recovery of specific phage and a substantial decrease in background. The BRASIL method is useful for identifying targeting peptides. The targeting peptides identified by the method of the invention are useful for treating disease states, such as:

disease, inflammatory arthritis, atherosclerosis; cancer, autoimmune disease, bacterial infection; viral infection; cardiovascular disease and
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Ч
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Biopanning and Rapid Analysis of Selective Interactive Ligands; dial
inflammatory arthritis; atherosclerosis; cancer; autoimmune disease
viral infection; cardiovascular disease; degenerative disease.
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2
                                                                                                                                                                   targeting peptide 49
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          degenerative disease. The present at targeting peptide of the invention
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larity 50.0%;
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Conservative
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17-JAN-2001;
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The invention comprises a method (BRASIL - Biopanning and Rapid Analysis of Selective Interactive Ligands) to obtain a targeting peptide. The BRASIL method of the invention involves: exposing a target to a phage display library in a first phase; exposing the first phase to a second phase; and separating the phage bound to the target from unbound phage. The BRASIL method of the invention allows cell phages to be separated from the remaining unbound phage in a single differential centrifugation step. When compared to conventional cell panning methods, the BRASIL method shows a significant increase in recovery of specific phage and a substantial decrease in background. The BRASIL method is useful for identifying targeting peptides. The targeting peptides identified by the method of the invention are useful for treating disease states, such as: diabetes; inflammatory arthritis; atherosclerosis; cancer; autoimmune disease; bacterial infection; viral infection; cardiovascular disease and cagenerative disease. The present amino acid sequence represents a cargeting peptide of the invention
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Biopanning and Rapid Analysis of Selective Interactive Ligands; diabinflammatory arthritis; atherosclerosis; cancer; autoimmune disease; viral infection; cardiovascular disease; degenerative disease.
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Pred. No. 1.7e+06;
); Mismatches 2
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17-JAN-2001; 2001US-00765101
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 standard; peptide;
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                       Fluorine-18
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activity
lung,
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                                                                                                                    factor;
diabetic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes an isolated peptide (I) that binds to inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I) have cytostatic, hepatotropic, antiinflammatory, hypotensive, antidiabetic and vulnerary activities, and can be used in gene therap Compositions and methods from the present invention are useful for diagnosing, evaluating and treating disorders mediated by the activit the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung, liver, spleen, kidney, lymph node, small intestine, blood cells, pancreas, colon, stomach, breast, endometrium, prostate, testicle, ov skin, head and neck, oesophagus, bone, marrow or blood, and diseases skin, head and neck, oesophagus, bone, marrow or blood, and post-trauma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           skin, head and neck, oesophagus, bone, marrow or blood, and disease neovascularisation, e.g. liver diseases, hypertension, post-trauma, chronic hepatitis, haemangiomas and diabetes. The present sequence represents a specifically claimed VEGFR-3 binding peptide from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or
                                                                                          Vascular endothelial growth factor receptor 3 inhibitor; VEGFR angiogenesis; vascular endothelial growth factostatic; hepatotropic; antiinflammatory; hypotensive; antid vulnerary; cell surface receptor; cancer; neovascularisation; liver disease; hypertension; post-trauma; chronic hepatitis; h diabetes; PDGF; platelet derived growth factor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated peptide that inhibits VEGF-C and VEGF-D, useful diagnosing, evaluating, treating disorders mediated by VEGFR such as cancer and diseases of neovascularization.
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                                                                                                                                                                                                                                                                                                           4. .6 /note= "X is any amino acid"
                                                          VEGFR-3 binding peptide SEQ ID NO:67.
                                                                                                                                                                                                                                                                                        Location/Qualifiers
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larity 57.1%;
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Misc-difference
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Synthetic.
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<del>Q</del>
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The invention relates to a method for incorporating 18F radionuclide into peptide-containing targeting vectors for use in clinical positron emission tomography. Radiolabeling thiol-containing peptides with fluorine-18 (F-18) comprises reacting a peptide comprising a free thiol group with a labeling reagent of formula: 18F-(CH2)m-CR1R2-(CH2)n-X, or a fluorinated alkene in which at least one of the two double bonded carbon atoms bars at least one leaving group comprising I, Br, Cl, azide, tosylate, mesylate, nosylate, mesylate, nosylate, mesylate, nosylate, mesylate, mesylate, nosylate, triflate, maleimide Coptionally substituted by 1-2 alkyl) or 3-sulfomaleimide; Rl, R2 = I, Br, Cl, azide, tosylate, mesylate, nosylate, triflate, H, CONH2, COOH, CH, sulfonic acid, tertiary ammonium, alkyl (optionally substituted by CONH2, COOH, OH, sulfonic acid, tertiary ammonium) cook, CONR'2 or COR'; and R' = 1-6C alkyl or phenyl. The method is used for Radiolabeling peptide-containing targeting vectors such as proteins, antibody fragments and receptortargeted peptides for use in routine clinical positron emission targeted peptides for use in routine clinical positron emission targeted peptides for use in routine clinical positron emission targeted property of the free thiol groups which are rapidly alkylated at neutral pH and moderate temperature. Sequences AAY03714-716 represent examples of F-18 labeled peptides used in the method of detecting a
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vector; positron emission tomography; F-18
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protected thiol group"
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Pred. No. 1.7e+06;
0; Mismatches 0;
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protected thiol group"
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18F radionuclide; targeting vector radiolabeling; thiol; fluorine-18.
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100.0%; Pi
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98US-0104156P
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                     AAY76817 standard; peptide;
                                        entry)
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14-OCT-1998;
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                                                                                                                                                                                                                                       conjugates
                                                                       Synthetic
                               AAY76817;
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Matches
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ABP5396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents an immunogenic peptide for a bi-specific antibody. The invention relates to a method of treating or identifying diseased tissues in a patient comprising administering a bi-specific attibody (or fragment) having at at least 1 arm (A) that specifically binds a targeted tissue and at least 1 arm (B) that specifically binds a targetable conjugate. The methods and bi-specific antibodies and fusion proteins are useful for pre-targeting methods of diagnosis and therapy. It is advantageous to raise bi-specific antibodies against a targetable conjugate that is capable of carrying at least 1 diagnostic or therapeutic agent or diagnostic agent can be varied to accommodate differing applications without raising new bi-specific antibodies for each new application. The targetable conjugate is selected to elicit sufficient immune responses and also for rapid in vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           is selected
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and fusion
i therapy.
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                                                                                                                                    response;
                                                                                                                                                                                                                                           a metal
                                                                                                                                                                                                                                                                                                                                    /note= "D-form residue; modified with free amino acid
group, protected amino acid group, chelating agent or
metal-chelate complex"
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                                                                                                                                                                                                                            modified with free amino a
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                                                                                                                                 Immunogenic peptide; bi-specific antibody; diagnosis; immune diseased tissue identification; therapy.
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                                                                                                        Immunogenic peptide for bi-specific antibody recognition.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -specific antibodies that bind specific target
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                                                                                                                                                                                                                            /note= "acetylated; modified
protected amino acid group,
chelate complex"
                                                                                                                                                                                                                                                                                                            "D-form residue"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3; angiogenesis; lymphangiogenesis; vascular endothelial growth factor; cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic; vulnerary; cell surface receptor; cancer; neovascularisation; liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma; diabetes; PDGF; platelet derived growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ovary,
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                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated peptide that inhibits VEGF-C and VEGF-D, useful for diagnosing, evaluating, treating disorders mediated by VEGFR-3 as such as cancer and diseases of neovascularization.
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   Length
 Score 33; DB 3; Pred. No. 1.7e+06; Mismatches 0
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45.8%;
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                                                                                                                                                                                                                                                                standard; peptide;
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                                                 Conservative
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                          Similarity 4; Conserv
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                                                                                                                                  CGYW
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                                                                                               CGYW
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                                                                                                                                                                                                                                         multi-specific antibody; polymer conjugat
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Score 33; DB 5; Le
Pred. No. 1.7e+06;
; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                       residue"
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a multi-specific antibody
that binds to the capture
                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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  45.8%;
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residue"
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Modified-site
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                                                                                                                                                                                                                Immunogenic
                                                                                                                                                                                                                                        Immunogenic cytostatic;
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ADG94005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a multi-specific and a capture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a method of diagnosing or treating a disease or disorder. The method involves administering to a tissue a multi-specific antibody (I) or antibody fragment, comprising a targeting arm that binds to an antigen on the target site, and a capture arm that binds to a
                     Gapa
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methylated; N-terminal acetylated.
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methylated; N-terminal acetylated.
Score 33; DB 7; L. Pred. No. 1.7e+06; ); Mismatches 0;
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c intiamentory disease, neurosegenerative diseases, metabolic disease;

c forms of B-cell lymphomas, aggressive forms of B-cell lymphomas, chirched control of the solid tumour is chosen melanoma, carcinoma (prefarbly renal carcinoma, lungs carcinoma, integrinal carcinoma, and stomach, carcinoma (prefarbly renal carcinoma, lungs carcinoma, integrinal carcinoma, and stomach, carcinoma (prefarbly renal carcinoma, lungs carcinoma, integrinal carcinoma, and stomach, carcinoma (prefarbly renal carcinoma, lungs carcinoma, integrinal lissue chosen from endometrium, thymnic splene and parathyroid. The method can be used for normal tissue ablation, where the antibody binds amyloid. The disease or disorder is an autoinmune disease such as manned and parathyroid. The method can be used for normal tissue ablation, where the tissue is chosen from bene marrow and spleen. The disease or disorder is an autoinmune mediated thrombocytopenia gravity and control follopathic thrombocytopenic purpura and chronic follopathic thrombocytopenia gravities, and rheumatoid architis, such autoimmune disease such as immune—mediated thrombocytopenia such an autoimmune disease such as immune—mediated thrombocytopenia such control anophritis, objective mediated thrombocytopenia such control anophritis, and theumatoid architis, sarcoidosis, ulcerative colscipation of disease wellitus, polympositis objectic such proposition, disbetes mellitus, extreme molecula nephropathy and colscipation of disease, rheumatoid architis, sarcoidosis, ulcerative colscipation of disease, rheumatoid architis, polymyositis dever, polygiandia spinia, polymyositis dever, polygiandia such propositis, polymyositis dever, polygian ulcerative colscipation of disease, rheumatoid architis, polymyositis dever, polygiandia such propositis, polymyositis, dever, polygian ulcerative colscipation of disease, results and receival and receival, polymyositis, dever, polygian volgian vilagia, pernosis, polymyositis, aused Boma gondii, Trypanosoma rangeli , Trypanosoma cruzi, Trypanosoma rhodesiensei, Trypanosoma brucei, Schistosoma mansoni, Schistos japanicum, Babesia bovis, Elmeria tenella, Onchocerca volvulus, Leishmania tropica, Trichinella spiralis, Onchocerca volvulus, parva, Taenia hydatigena, Taenia ovis, Taenia saginata, Echinoc granulosus, and Mesocestoides corti. The infectious disease is a mycoplasma chosen from Mycoplasma arthritidis, M. hyorhinis, M. arginini, Acholeplasma laidlawii, M. salivarum and M. pneumo cancer is preferably chosen from carcinoembryonic antigen (CEA) expressing tumour or a CD20-expressing malignancy. The present represents a peptide used in the method of the invention.

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The invention relates to modulating agents for inhibiting or enhancing desmosomal cadherin mediated cell adhesion, comprising a modulating agent comprising a desmosomal cadherin cell adhesion recognition CAR sequence (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR sequence, a substance such as an antibody or antigen-binding fragment that specifically binds a desmosomal cadherin CAR sequence and/or a polynucleotide encoding a polypeptide that comprises a desmosomal cadherin CAR sequence or analogue. The modulating agents have immunosuppressive, cytostatic and antiapoptotic activity and are used to facilitate wound healing and/or reduce scar tissue, for enhancing adhesion of foreign tissue implants (e.g. skin graft or organ implant), treating an autoimmune blistering disorder and to treat cancer (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis
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GENERAL INFORMATION:
APPLICANT: Blachuk, Orest W.
APPLICANT: Symonds, James M.
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND EMTHODS FOR MODULATING
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                                                                                                                                    FILE REFERENCE: 100086.407C6
CURRENT APPLICATION NUMBER: US/09/535,852
CURRENT FILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 2009
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1090
LENGTH: 10
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                                                                                                                                                                                                                                                                                                                                                                        Similarity 6; Conserv
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OTHER INFORMATION:
9-535-852-1090
US-09-535-852-1090
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Best Local S
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3-09-535-
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Sequence 1352, Application US/09535852
; Sequence 1352, Application US/09535852
; GENERAL INFORMATION:
; APPLICANT: Blachuk, Orest W.
; APPLICANT: Symonds, James M.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND EMTHODS FOR MODULATING;
; TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C6
; CURRENT APPLICATION NUMBER: US/09/535,852
; CURRENT FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 2009
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1352
; LENGTH: 10 SULT 2 -09-535-852-1352 RESULT US

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Similarity 100
4; Conservative
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ADDRESSEE:
STREET: 43
CITY: San
STATE: Cal
COUNTRY: U
                                                                    92122
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US-09-079-432-12
; Sequence 12, Application US/09079432
; Patent No. 5955572
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Structural Mimics of RGD-Binding Sites
; NUMBER OF SEQUENCES: 28
                                                                                                                                                                                                                                                                         APPLICANT: Ruoslahti, Erkki
APPLICANT: Pasqualini, Renata
TITLE OF INVENTION: Structural Mimics of RGD-Binding Sites
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                              comprising
recognition
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/520,535
FILING DATE: 28-AUG-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 1794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-8949
INFORMATION FOR SEQ ID NO: 12:
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Pred. No. 3.8e+05;
); Mismatches 1;
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                             modulating agent
1-1 cell adhesion
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                                                                                  Score 33; DB Pred. No. 81; 0; Mismatches
                                                                                   DB
81;
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US-08-520-535-12
; Sequence 12, Application US/0852053:
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  ORGANISM: Artificial Sequence
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Similarity 80.0%;
4; Conservative
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Similarity 60.0%;
6; Conservative
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   amino acid
   AMINO acid
GY: circular
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California
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GENERAL INFORMATION:
APPLICANT: Ruoslah
                          OTHER INFORMATION:
OTHER INFORMATION:
US-09-535-852-1352
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CITY: SE
STATE: Calir
COUNTRY: USI
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US-08-520-535-12
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TYPE: am
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RESULT 5
US-08-986-234-92
US-08-986-234-92
; Sequence 92, Application US/08986234
; Patent No. 5981706
; GENERAL INFORMATION:
; APPLICANT: Wallen, et al.
; TITLE OF INVENTION: Methods for Synthesizing Heat Shock Protein Complexes
; FILE REFERENCE: UNME-0008-1
; CURRENT APPLICATION NUMBER: US/08/986,234
; CURRENT FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 92
; LENGTH: 9
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                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,432
FILING DATE:
CLASSIFICATION NUMBER: US 08/520,535
FILING DATE:
APPLICATION NUMBER: US 08/520,535
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: P-LA 1794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-9001
TELEFAX: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Les
3.8e+05;
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3.8e+05;
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                   Suite 700
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SSEE: Campbell & Flores LLP
[: 4370 La Jolla Village Drive,
San Diego
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 30;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Human immunodeficiency virus
US-08-986-234-92
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Sequence 22, Application US/09108709
; Sequence 22, Application US/09108709
; Patent No. 6008044
; GENERAL INFORMATION:
; APPLICANT: Cortropia, Joseph P.
; TITLE OF INVENTION: (gp41) of Human Immunodeficiency Virus-1 (HIV-1) and Prognosis T-
; TITLE OF INVENTION: (gp41) of Human Immunodeficiency Virus-1 (HIV-1) and Prognosis T-
; TITLE OF INVENTION: (gp41) of Human Immunodeficiency Virus-1 (HIV-1) and Prognosis T-
; TITLE OF INVENTION: (gp41) of Human Immunodeficiency Virus-1 (HIV-1) and Prognosis T-
; TITLE OF INVENTION: (sp6/00406
; TITLE OF INVENTION: Fusion-associated Epitope (GCSGKLIC) in gp-41
; FILE REFERENCE: 10586/00406
; CURRENT APPLICATION NUMBER: US/09/108,709
; CURRENT FILING DATE: 1998-07-01
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 22
LENGTH: 10
; TYPE: PRT

ORGANISM: Human immunodeficiency virus type 1
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TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR USE IN
A PROCESS FOR DETERMINATION OF ANTIBODIES OF
BIOTINYLATED PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTAN'S
EPITOPES, A PROCESS FOR PREPARING THEM AND COMPOSITIONS
CONTAINING THEM
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TITLE OF INVENTION: BIOTINYLATED PEPTIDES CC
TITLE OF INVENTION: EPITOPES, A PROCESS FOR
TITLE OF INVENTION: CONTAINING THEM
FILE REFERENCE: 2752-16
CURRENT APPLICATION NUMBER: US/09/790,497A
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 09/576,824
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Pred. No.
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PRIOR APPLICATION NUMBER: 08/723,425
PRIOR FILING DATE: 1996-09-30
PRIOR APPLICATION NUMBER: 09/146,028
PRIOR FILING DATE: 1993-11-22
PRIOR APPLICATION NUMBER: PCT/EP93/005:
PRIOR FILING DATE: 1993-03-08
PRIOR APPLICATION NUMBER: EP 92400598.6
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Patent No. 6649735
GENERAL INFORMATION:
APPLICANT: De Leys, Robert
TITLE OF INVENTION: PROCESS FOR THE DI
TITLE OF INVENTION: TO IMMUNOLOGICALI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: amino acids 600-(OTHER INFORMATION: numbering system 09-108-709-22
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Conservative (
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SOFTWARE: PatentIn Ver. 2.1
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Best Local Similarity
Matches 4; Conser
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US-09-790-497A-110
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       APPLICANT: Fikes, John D.
APPLICANT: Hermanson, Gary G.
APPLICANT: Sette, Alessandro
APPLICANT: Sette, Alessandro
APPLICANT: Livingston, Brian
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert W.
APPLICANT: Epimmune Inc.
ITILE OF INVENTION: Expression Vectors for Stimulating an
ITILE OF INVENTION: Immune Response and Methods of Using the
FILE REFERENCE: 39963-20022.01
CURRENT APPLICATION NUMBER: US/09/311,784A
CURRENT FILING DATE: 1999-05-13
PRIOR FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 463
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 374
LENGTH: 9
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Mismatches 0;
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Patent No. 6649735
GENERAL INFORMATION:
APPLICANT: De Leys, Robert
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NUMBER OF SEQ ID NOS: 600
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: HIV1 ENV
US-09-311-784A-374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.v
INFORMATION:
NT: Fikes, John D.
NT: Hermanson, Gary
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Best Local Similarity
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US-09-790-497A-1
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Best Local Similarity
Matches 3; Conser
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TOPOLOGY: 11:
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APPLICANT: Franz, Gerald H.
APPLICANT: Loukeris, Athanasios
TITLE OF INVENTION: Eukaryotic Transposable Element
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                             Transposable Element
                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/946,237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 29; DB 1; Louis Pred. No. 3.8e+05; L; Mismatches 0;
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 19920914
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: David E. Brook
REGISTRATION NUMBER: 22,592
REFERENCE/NOWNER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22,592
3R: BTT92-01
                                                                                                                                                                  APPLICANT: Savakis, Charalambos
APPLICANT: Franz, Gerald H
APPLICANT: Loukeris, Athanasios
TITLE OF INVENTION: Eukaryotic T
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10, Application US/08530566
Patent No. 5840865
GENERAL INFORMATION:
                                                                                                          US-07-946-237-4
; Sequence 4, Application US/07946237
; Patent No. 5348874
                                                                                                                                                                    Charalambos
                                                                                                                                                                                               Athanasios
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                                                                                                                                                                                                                                                     Brook,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: BT'
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
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illarity 75.0%;
Conservative
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STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECULULATION: (617) BOL-VERINFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
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Conservative
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Massachusetts
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Best Local Similarity
Matches 3; Conser
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                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Savaki
                           IWGC 10
                                                                                                                                                                                                                                                                                                           USA
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US-08-530-566-10
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                                                                                                                                                                                                                                                                                CITY: I
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                                                                                           Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ore 29; DB 2;
ed. No. 3.8e+05;
Mismatches 0
                                    MEDIUM TIPE: FIOPPY GIBK
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Versi
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/530,566
FILING DATE: 20-SEP-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/239,765
FILING DATE: 09-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/946,237
FILING DATE: 14-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: BTT92-01ZA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 29;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/530,566
FILING DATE: 20-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/239,765
FILING DATE: 09-MAY-1994
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Vacurrent APPLICATION DATA:

APPLICATION NUMBER: US/09/195,726
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US-09-195-726-10
; Sequence 10, Application US/09195726
; Patent No. 6159717
; GENERAL INFORMATION:
; APPLICANT: Savakis, Charalambos
; APPLICANT: Franz, Gerald H.
APPLICANT: Loukeris, Athanasios
; TITLE OF INVENTION: Eukaryotic TrannumBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
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Conservative
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Conservative
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COMPUTER READABLE FORM:
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STATE: D.C.
COUNTRY: U.S.A.
                                                           peptide
    ; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: pepti
US-09-067-755-10
                                                                                                                              Local Similarity
nes 3; Conser
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OTHER INFORMATION:
US-08-239-765C-4
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ORGANISM: Unknown
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VWGC
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-239-765C-4
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SOFTWARE: Pr
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APPLICANT: Franz, Gerald H.
APPLICANT: Loukeris, Athanasios
APPLICANT: Klinakis, Apostolos G.
TITLE OF INVENTION: Eukaryotic Transposable Element
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/067,755
FILING DATE: 27-APR-1998
CLASSIFICATION BOTA:
APPLICATION NUMBER: US 08/530,566
FILING DATE: 20-SEP-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                      Score 29; DB 3; L. Pred. No. 3.8e+05; l; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3: Hamilton, Brook, Smith & Reynolds,
Two Militia Drive
APPLICATION NUMBER: US 07/946,237
FILING DATE: 14-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Alice O.
REGISTRATION NUMBER: 33,542
REFERENCE/DOCKET NUMBER: IMBB92-012AZ
TELEPHONE: (781) 861-6240
TELEPHONE: (781) 861-9540
TELEFAX: (781) 861-9540
TYPE: amino acids
TYPE: amino acids
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FILING DATE: 09-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/946,237
FILING DATE: 14-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Alice O.
REGISTRATION NUMBER: 33,542
REFERENCE/DOCKET NUMBER: IMBB92-0122
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10, Application US/09067755
o. 6225121
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                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 75.0%;
Matches 3; Conservative
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STREET: Two Milit
CITY: Lexington
STATE: Massachus
COUNTRY: USA
ZIP: 02421
                                                                                                                                                                                                                                                    linear
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Patent No. 6225121
GENERAL INFORMATION:
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MOLECULE TYPE:

US-09-195-726-10
                                                                                                                                                                                                                                STRANDEDNESS
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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Length
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  DB 3;
3.8e+05;
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Pred. No. 3.8e+05
; Mismatches
DB 3
                                                                                                                                  Sequence 4, Application US/08239765C; Patent No. 6469228; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Savakis, Charalambos
APPLICANT: Franz, Gerald H
APPLICANT: Loukeris, Athanasios
TITLE OF INVENTION: Eukaryotic Transposable F
FILE REFERENCE: 18747/1130
CURRENT APPLICATION NUMBER: US/08/239,765C; CURRENT FILING DATE: 1994-05-09
PRIOR APPLICATION NUMBER: 07/946,237
PRIOR FILING DATE: 1992-09-14
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
                        Mismatches
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29;
No.
Score
Pred. 1
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; Sequence 94, Application US/09069827A
; Patent No. 6617114
; GENERAL INFORMATION:
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Pred. No. 3.8e+05;
0; Mismatches 3;
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/069,827A
FILING DATE: 30-Apr-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION NUMBER: US 09/050,359
FILING DATE: 31-MAR-1997
APPLICATION NUMBER: US 08/740,671
FILING DATE: 31-OCT-1997
APPLICATION NUMBER: US 08/740,671
FILING DATE: 31-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVET P
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: FOWLKES=4C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acids
US-09-069-827A-94
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Best Local Similarity 57.1%;
Matches 4; Conservative
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Search completed: December 30, 2004, 14:44:16 Job time : 24.6667 secs

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Sequence 35, Appl Sequence 34, Appl Sequence 73, Appl Sequence 67, Appl Sequence 1090, Appl Sequence 1352, Ap Sequence 39, Appl Sequence 39, Appl Sequence 36, Appl Sequence 36, Appl Sequence 1454, Appl Sequence 78, Appl Sequence 78, Appl
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2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

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US-10-654-578-1352

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US-10-046-922-35

i Sequence 35, Application US/10046922

j Publication No. US20020164667A1

i GENERAL INFORMATION:

i APPLICANT: Alitalo, Kari

i APPLICANT: Kubo, Hajime

i TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS

i FILE REFERENCE: 28967/37084A

i CURRENT FILING DATE: 2002-01-15

i SOFTWARE: Patentin version 3.0

i SEQ ID NO 35

i LENGTH: 10
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US-09-894-018-185
US-10-303-331-104
US-10-371-525-374
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US-10-371-569-374
US-10-371-260-374
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US-10-474-960A-185
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US-10-371-260-348
US-10-371-525-348
US-10-371-645-348
US-10-371-645-348
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US-10-182-252A-181
US-10-182-252A-1271
US-09-947-925A-21
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0.0026;
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   ORGANISM: isolated peptide -10-046-922-35
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RESULT 2
US-10-046-922-34
; Sequence 34, Application US/10046922
; Publication No. US20020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Koivunen, Erkki

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Best Local Similarity 57.1%;
Matches 4; Conservative
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; LOCATION: (4)..(6)
; OTHER INFORMATION: X i
; NAME/KEY: SITE
; LOCATION: (8)..(8)
; OTHER INFORMATION: X i
US-10-046-922-68
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Best Local Similarity
Matches 4; Conser
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; OTHER INFORMATION:
US-10-046-922-67
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TYPE: PRT
ORGANISM: peptide
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ORGANISM: peptide
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US-10-654-578-1090
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US-10-046-922-73
US-10-046-922-73
; Sequence 73, Application US/10046922
; Publication No. US20020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Kubo, Hajime
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
; FILE REFERENCE: 28967/37084A
; CURRENT APPLICATION NUMBER: US/10/046,922
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
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Pred. No. 0.72;
); Mismatches
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TITLE OF INVENTION: VEGFR-3 INHIBITOR MATER]
FILE REFERENCE: 28967/37084A
CURRENT APPLICATION NUMBER: US/10/046,922
CURRENT FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin version 3.0
SEQ ID NO 34
TYPE- TITLE
TYPE-
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Publication No. US20020164667A1
GENERAL INFORMATION:
APPLICANT: Alitalo, Kari
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Koivunen, Erkki
Kubo, Hajime
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ORGANISM: peptide library
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LOCATION: (1)..(1)
OTHER INFORMATION: X
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OTHER INFORMATION: 3
NAME/KEY: SITE
LOCATION: (9)..(9)
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NAME/KEY: SITE
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LENGTH: 10
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APPLICANT:
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TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS FILE REFERENCE: 28967/37084A CURRENT APPLICATION NUMBER: US/10/046,922 CURRENT FILING DATE: 2002-01-15 NUMBER OF SEQ ID NOS: 80 SOFTWARE: Patentin version 3.0 SEQ ID NO 67 LENGTH: 7
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APPLICANT: Symonds, James Matthew
APPLICANT: Symonds, James Matthew
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 100086.407C10
CURRENT APPLICATION NUMBER: US/10/654,578
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ed. No. 1.5e+06;
Mismatches 3
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Pred. No. 1.5e+06;
Mismatches
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US-10-046-922-68
; Sequence 68, Application US/10046922
; Publication No. US20020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Koivunen, Erkki
; APPLICANT: Kubo, Hajime
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERI
; FILE REFERENCE: 28967/37084A
; CURRENT APPLICATION NUMBER: US/10/046,922
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 68
; LENGTH: 8
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Pred. No.
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APPLICATION NUMBER:
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ENGTH: 10
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                                                                                                                                                                                     Length 10;
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APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 100086.407C10
CURRENT APPLICATION NUMBER: US/10/654,578
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5e+02;
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No. 5e+02;
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Pred. No. 5e+0.
0; Mismatches
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APPLICANT: Grey, Howard M.
APPLICANT: Sette, Alessandro
APPLICANT: Celis, Esteban
TITLE OF INVENTION: HLA Binding Peptides and
FILE REFERENCE: 2060.005000A
CURRENT APPLICATION NUMBER: US/08/821,739A
CURRENT FILING DATE: 1999-03-20
PRIOR APPLICATION NUMBER: 60/013,833
PRIOR FILING DATE: 1996-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 2003-09-03
NUMBER OF SEQ ID NOS: 2009
SOFTWARE: FastSEQ for Windows Version 4.0
EQ ID NO 1352
LENGTH: 10
2003-09-03
2009
Windows Version
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US-08-821-739A-90
; Sequence 90, Application US/08821739A
; Publication No. US20020168374A1
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
                                                                                                                                                                                                                                                                                                                                        3-10-654-578-1352
Sequence 1352, Application US/10654578
Publication No. US20040229811A1
GENERAL INFORMATION:
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FILING DATE: 1996-07-12
APPLICATION NUMBER: 08/451,913
FILING DATE: 1995-05-26
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                                                                                        ORGANISM: Artificial Sequence
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larity 60.0%;
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FILING DATE:
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nes 6; Conser
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OTHER INFORMATION:
US-10-654-578-1352
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APPLICANT: Symonds
APPLICANT: Gour, B
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                                            SEQ ID NO 1090
LENGTH: 10
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Matches 6
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APPLICANT: DeLisi, Charles
APPLICANT: Berzofsky, Jay
APPLICANT: Berzofsky, Jay
APPLICANT: Berzofsky, Jay
APPLICANT: Gulukota, Kamalakar
APPLICANT: Vaccaro, Dennis
APPLICANT: Vaccaro, Dennis
APPLICANT: Vaccaro, Dennis
APPLICANT: Weng, Zhiping
APPLICANT: Vaccaro, Dennis
APPLICANT: ZONPOSITIONS THEREOF
FILE REFERENCE: BU-035AX
CURRENT APPLICATION NUMBER: US/10/133,210
CURRENT FILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 281
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 39
LENGTH: 10
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No. 6.8e+02;
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Pred. No. 6.8e+02
); Mismatches
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PRIOR FILING DATE: 1994-12-01
PRIOR APPLICATION NUMBER: 08/186,266
PRIOR FILING DATE: 1994-01-25
PRIOR APPLICATION NUMBER: 08/159,339
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: 08/103,396
PRIOR FILING DATE: 1993-08-06
PRIOR APPLICATION NUMBER: 08/027,746
PRIOR APPLICATION NUMBER: 08/027,746
PRIOR FILING DATE: 1993-03-05
PRIOR FILING DATE: 1993-03-05
NUMBER OF SEQ ID NOS: 149
SOFTWARE: Patentin version 3.1
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Pred.
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APPLICANT: DeLisi, Charles; APPLICANT: Berzofsky, Jay; APPLICANT: Gulukota, Kamalakar; APPLICANT: Vaccaro, Dennis
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nilarity 83.3%;
Conservative (
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ORGANISM: Artificial Sequence
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Best Local Similarity 83.3%;
Matches 5; Conservative
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Best Local Similarity
Matches 5; Conser
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APPLICANT: Sette, Alessandro
APPLICANT: Sette, Alessandro
APPLICANT: Celis, Esteban
TITLE OF INVENTION: HLA Binding Peptides and Their Uses
FILE REFERENCE: 2060.005000A
CURRENT APPLICATION NUMBER: US/08/821,739A
CURRENT FILING DATE: 1999-03-20
PRIOR APPLICATION NUMBER: 60/013,833
PRIOR FILING DATE: 1996-03-21
PRIOR APPLICATION NUMBER: 08/589,107
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APPLICANT: Tijerina, Pilar
TITLE OF INVENTION: METHODS FOR SELECTIVE TARGETING
FILE REFERENCE: GC617-2
CURRENT APPLICATION NUMBER: US/09/832,723
CURRENT FILING DATE: 2001-04-11
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                                                   Score 31; DB 10;
Pred. No. 9.3e+02,
Mismatches
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Pred. No.
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R APPLICATION NUMBER: 08/451,913

R FILING DATE: 1995-05-26

R APPLICATION NUMBER: 08/347,610

R FILING DATE: 1994-12-01

R APPLICATION NUMBER: 08/186,266

R APPLICATION NUMBER: 08/186,266

R APPLICATION NUMBER: 08/159,339

R APPLICATION NUMBER: 08/103,396

R APPLICATION NUMBER: 08/103,396

R APPLICATION NUMBER: 08/103,796

R APPLICATION NUMBER: 08/103,796

R APPLICATION NUMBER: 08/027,746

R APPLICATION NUMBER: 08/027,746
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NUMBER OF SEQ ID NOS: 149
SOFTWARE: Patentin version 3.1
SEQ ID NO 78
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Sequence 78, Application US/08821739A
Publication No. US20020168374A1
GENERAL INFORMATION:
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US-09-832-723-104
; Sequence 104, Application US/09832723
; Patent No. US20020098524A1
; GENERAL INFORMATION:
; APPLICANT: Estell, David A.
; APPLICANT: Chen, Yiyou
 ; OTHER INFORMATION: in this patent. US-09-572-404B-1454
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                                                  Similarity 62.5%; Similarity 62.5%; 5; Conservative
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4; Conservative
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APPLICANT: Weng, Zhiping
APPLICANT: Zhang, Chao
TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND
TITLE OF INVENTION: COMPOSITIONS THEREOF
FILE REFERENCE: BU-035AX
CURRENT APPLICATION NUMBER: US/10/133,210
CURRENT FILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 281
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-572-404B-1454

US-09-572-404B-1454

Sequence 1454, Application US/09572404B

Publication No. US20030078374A1

GENERAL INFORMATION:

APPLICANT: Proteom Ltd

TITLE OF INVENTION: Complementary peptide ligands from the human

FILE REFERENCE: Human patent

CURRENT APPLICATION NUMBER: US/09/572,404B

CURRENT FILING DATE: 2000-05-17

NUMBER OF SEQ ID NOS: 4203

SOFTWARE: ProtPatent version 1.0

SEQ ID NO 1454

LENGTH: 10
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; Publication No. US20020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Kubo, Hajime
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
; FILE REFERENCE: 28967/37084A
; CURRENT APPLICATION NUMBER: US/10/046,922
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: Patentin version 3.0
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Pred. No. 1.5e+06;
0; Mismatches 3;
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Pred. No. 6.8e+02;
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OTHER INFORMATION: sequence located in P2RYS
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ORGANISM: Artificial Sequence
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larity 83.3%;
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; OTHER INFORMATION: peptides screened from a phage display random
; OTHER INFORMATION: peptide library
US-09-832-723-104
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US-09-894-018-80
; Sequence 80, Application US/09894018
; Patent No. US20020119127A1
; GENERAL INFORMATION:
; APPLICANT: EPINMUNE, Inc.
; APPLICANT: Gette, Alessandro
; APPLICANT: Chestnut, Robert
APPLICANT: Livingston, Brian
APPLICANT: Livingston, Brian
APPLICANT: Baker, Denisw
; PRICANT: Brown, David
; TITLE OF INVENTION: MINICENES AND PEPTIDES THEREBY
; FILE REFERENCE: 39963-20033.00
; CURRENT APPLICATION NUMBER: US/09/894,018
; CURRENT APPLICATION NUMBER: US 60/173,390
; PRIOR FILING DATE: 2001-06-27
; PRIOR FILING DATE: 1999-12-28
; PRIOR FILING DATE: 1999-12-28
; PRIOR FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 80
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Pred. No. 1.5e+06;
0; Mismatches 0;
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Pred. No. 1.5e+06;
0; Mismatches 4
PRIOR APPLICATION NUMBER: US 60/197,259
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 117
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 104
LENGTH: 9
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Matches 4; Conservative 0;
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llarity 50.0%;
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protein search, using sw model OM protein

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tes/sec ; Search time 18.6667 S (without alignments) 51.545 Million cell upda

US-10-046-922-35 CGYWLTIWGC 10 Title: Perfect score: Sequence:

Scoring table:

283416 segs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

1102 Total number of hits satisfying chosen parameters:

Minimum DB seg length: 0

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:* 4 0 6 4

re a printed, Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being and is derived by analysis of the total score distribution.

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ALIGNMENTS

RESULT 1	
ase (EC 2.5.1.18) clas lutathione S-transfers	
C;Species: Sus scrofa domestica (domestic pig) C;Date: 19-Mar-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004 C;Accession: S71868	
R;Rouimi, P.; Anglade, P.; Debrauwer, L.; Tulliez, J. Biochem, J. 317, 879-884, 1996	
n of pig liver glutathione S-transferases using 64: MUID:96332484: PMID:8760377	HPLC-electrospra
A;Molecule type: procein A;Residues: 1-10 <rou></rou>	
ROT:Q7M3E8 species-independent classes of cytosolic glutathion	transferasc
A;Description: catalyzes the nucleophilic conjugation of intracellular glutathione A;Pathway: detoxification; xenobiotics metabolism	ne to a
A; Note: increased hydrophilicity of GSH-conjugates facilitates their further metabolism	abolism
es or damage C;Superfamily: glutathione transferase C;Keywords: dimer; transferase	
Query Match Best Local Similarity 100.0%; Pred. No. 9.9e+02; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy 2 GYW 4	
Db 4 GYW 6	
RESULT 2 A35556 hypothetical protein (ODC region) - human	
C;Date: 21-Sep-1990 #sequence_revision 21-Sep-1990 #text_change 30-Sep-1993	
cunca, M.; Dosescu, J.; Almodovar, K.M.; Luk,	G.D.
ion and expressions: A35556; MUID	
A;Accession: A33339 A;Status: preliminary; not compared with conceptual 'translation A;Molecule type: DNA	
A;Residues: 1-10 <mos> A;Cross-references: GB:J05271</mos>	

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larity 40.0%;
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A; Accession: E41946
A; Status: preliminary; not of A; Molecule type: DNA
A; Residues: 1-10 <WHE>
C; Keywords: T-cell receptor
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: E41946
R;Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; K]
Mol. Cell. Biol. 11, 5902-5909, 1991
A;Title: Rearrangement and junctional-site sequence analyses of T-cell receptive ference number: A41946; MUID:92049316; PMID:1658619
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R; Macey, J.R.; Larson, A.; Ananjeva, N.B.; Papenfuss, T.J. J. Mol. Evol. 44, 660-674, 1997
A; Title: Evolutionary shifts in three major structural features A; Reference number: Z18674; MUID: 97315309; PMID: 9169559
A; Accession: T17075
A; Accession: T17075
A; Molecule type: DNA
A; Molecule type: DNA
                                                                                                                                                    T-cell receptor beta chain V-D-J region (141-1CN) - mouse (fraging Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change
C; Accession: PT0586; PT0592
R; Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A; Title: Junctional sequences of fetal T cell receptor beta cha: A; Reference number: PT0509; MUID: 91277601; PMID:1711558
A; Accession: PT0586
A; Status: translation not shown
A; Molecule type: mRNA
A; Residues: 1-7 <FEE>
A; Residues: 1-7 <FEE>
A; Experimental source: day 19 fetal thymus, strain BALB/c (clone C; Keywords: T-cell receptor
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Pred. No. 2.8e+05;
1; Mismatches 0;
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7
 Pred. No. 9.9e+02; Mismatches
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Pred. No. 2e+03;
); Mismatches
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C;Keywords: mitochondrion; oxidoreductase
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S19288
acylase - Kluyvera cryocrescens
C;Species: Kluyvera cryocrescens
C;Species: Kluyvera cryocrescens
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S19288
C;Accession: S19288
R;Martin, J.; Slade, A.; Aitken, A.; Arche, R.; Virden, R.
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C; Species: Anguilla japonica (Japanese eel)
C; Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 11-Apr-C; Accession: JH0253
R; Uesaka, T:; Ikeda, T:; Kubota, I:; Muneoka, Y:; Ando, M.
Biochem. Biophys. Res. Commun. 180, 828-832, 1991
A; Title: Structure and function of a pentapeptide isolated from the gut A; Reference number: JH0253; MUID:92062113; PMID:1953755
A; Accession: JH0253
A; Molecule type: protein
A; Residues: 1-5 < UES>
A; Residues: This peptide increased basal tone of the circular muscle of t
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F41946
T-cell receptor gamma chain (1a.27) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-1
C;Accession: F41944 #sequence_revision 03-Feb-1994 #text_change 07-1
C;Accession: Rearrangement and junctional-site sequence analyses of T-c
Mol. Cell. Biol. 11, 5902-5909, 1991
A;Title: Rearrangement and junctional-site sequence analyses of T-c
A;Reference number: A41946; MUID:92049316; PMID:1658619
A;Accession: F41946
A;Accession: F41946
A;Ketus: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-6 <WHE>
C;Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ő
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 translation
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Comment: This peptide increased basal tone of the circular m
and of the circular muscle of the gastro-intestinal junction
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Pred. No. 2.8e+05;
1; Mismatches 0;
                                                                                                                                     Score 21; DB 2; Lo Pred. No. 2.8e+03; .; Mismatches 2;
not compared with conceptual
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T-cell receptor gamma chain V-D-J region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Dec-1993 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
C;Accession: F49033
R;Morita, C.T.; Verma, S.; Aparicio, P.; Martinez, C.; Spits, H.; Brenner, M.B.
Eur. J. Immunol. 21, 2999-3007, 1991
A;Title: Functionally distinct subsets of human gamma/delta T cells.
A;Reference number: A49033; MUID:92083926; PMID:1684157
A;Accession: F49033
A;Accession: F49033
A;Accession: F49033
A;Cross-references: DNA
A;Residues: 1-10 <MOR>
A;Cross-references: GB:S72605; NID:g240700; PIDN:AAB20632.1; PID:g240701
C;Keywords: T-cell receptor
 C; Accession: E49033; D49033
R; Morita, C.T.; Verma, S.; Aparicio, P.; Martinez, C.; Spits, H.; Brenner, M. Eur. J. Immunol. 21, 2999-3007, 1991
A; Title: Functionally distinct subsets of human gamma/delta T cells.
A; Reference number: A49033; MUID:92083926; PMID:1684157
A; Accession: E49033
A; Residues: 1-10 eMOR>
A; Molecule type: DNA
A; Residues: 1-10 eMOR>
A; Residues: Bequence extracted from NCBI backbone (NCBIN:72591, NCBIP:72595)
A; Note: sequence extracted from NCBI backbone (NCBIN:72591, NCBIP:72595)
A; Molecule type: DNA
A; Residues: 1-10 eMOR>
A; Residues: 1-10 eMOR>
A; Residues: 1-10 eMOR>
A; Cross-references: GB:S72587; NID:g240696; PIDN:AAB20630.1; PID:g240697
A; Molecule type: DNA
A; Residues: 1-10 eMOR2>
A; Residues: 1-10 eMOR2>
A; Note: sequence extracted from NCBI backbone (NCBIN:72587, NCBIP:72589)
C; Keywords: T-cell receptor
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PMID:1658619
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C41946
T-cell receptor gamma chain (1t.60) - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #tc
C; Accession: C41946
R; Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer,
Mol. Cell. Biol. 11, 5902-5909, 1991
A; Title: Rearrangement and junctional-site sequence as
A; Reference number: A41946; MUID:92049316; PMID:16586
A; Accession: C41946
A; Status: preliminary; not compared with conceptual to
A; Molecule type: DNA
A; Residues: 1-10 < WHE>
C; Keywords: T-cell receptor
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5.4e+03;
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5.4e+03;
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Pred. No. 5.4e+03
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Best Local Similarity 50.0%;
Matches 2; Conservative
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Best Local Similarity
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E49033
T-cell receptor gamma chain V-D-J region - human (fragment).
C;Species: Homo sapiens (man)
C;Species: 19-Dec-1993 #sequence_revision 25-Aug-1995 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aug-1996
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C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug
C; Accession: PT0289
R; Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; R
J. Exp. Med. 173, 395-407, 1991
A; Title: Preferential utilization of specific immunoglobulin heavy cha
A; Reference number: PT0222; MUID: 91108337; PMID:1899102
A; Accession: PT0289
A; Molecule type: DNA
A; Residues: 1-10 < YAM>
A; Experimental source: B lymphocyte
C; Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                Ignery chain CRD3 region (clone J2-106C) - human (fragment)
C;Species: Homo Bapiens (man)
C;Species: Homo Bapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug
C;Accession: PT0324
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; R
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy cha
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0324
A;Molecule type: DNA
A;Residues: 1-9 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin
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                            at the active; PMID:1764029
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Pred. No. 5.4e+03;
                                                                                                                                                                                              Score 20; DB 2; L. Pred. No. 2.8e+05; L; Mismatches 2;
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Mismatches 3;
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Pred. No.
   659-662, 1991
modification of serine at
er: S19288; MUID:92109664;
Biochem. J. 280, 659-662, 1991
A;Title: Chemical modification of se A;Reference number: S19288; MUID:921
A;Accession: S19288
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-8 <MAR>
A;Cross-references: UNIPROT:Q7M124
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C; Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C; Accession: JS0315
R; Holman, G.M.; Cook, B.J.; Nachman, R.J.
Comp. Biochem. Physiol. C 88, 27-30, 1987
A; Title: Isolation, primary structure, and synthesis of leucokinins V and V. A; Reference number: JS0315
A; Accession: JS0315
A; Molecule type: protein
A; Residues: 1-8 aHOL>
A; Residues: 1-8 aHOL>
A; Comment: Leucokinins, a family of cephalomyotropic peptides
C; Comment: Leucokinins, a family of cephalomyotropic peptide
C; Keywords: amidated carboxyl end; cephalomyotropic peptide
F; 8/Modified site: amidated carboxyl end (Gly) #status experimental
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C;Species: Homo Bapiens (man)
C;Species: Homo Bapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug
C;Accession: PT0230
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; R
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy cha
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0230
A;Molecule type: DNA
A;Residues: 1-10 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin
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US-10-046-922-35 72 Title: Perfect score:

CGYWLTIWGC 10 Sequence:

BLOSUM62 Gapop 10.0 , Gapext Scoring table:

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575374646 residues 1825181 segs, Searched:

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Maximum DB sequiength

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Database

UniProt_02:*
1: uniprot_grot:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Q8SHF6
Q8SHF6;
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Q1-JUN-2002 (TrEMBLrel. 21, Created)
O1-JUN-2002 (TrEMBLrel. 21, Last sequence update)
O1-JUN-2003 (TrEMBLrel. 25, Last annotation update)
O1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Cytochrome c oxidase subunit I (Fragment).
Name=COI;
Chamaeleo melleri (Meller's chameleon).
Mitochondrion.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleo.
NCBI_TaxID=179915;

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Bshe	8shf3 chamaeleo	Q8shf9 chamaeleo j	8shg5 chamaeleo	Q8shg8 chamaeleo g	Bshhl chamaeleo	8shh4 chamaeleo	8shh7 chamaeleo	Bshi	Q8shi3 chamaeleo c	Behi6 chamaeleo	Bshi	Behj	shj
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ALIGNMENTS

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STANDARD; PRT; 10 AA. el. 13, Created) el. 14, Last sequence update) el. 14, Last annotation update) fida (Physic nut). fida (Physic nut). idiplantae; Streptophyta; Embryophyta; Tracheophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; phighiales; Euphorbiaceae; Crotonoideae; Jatropheae; for Sluis W.G., Boelens R., T'Hart L.A., Labadie R.P.; novel cyclic decapeptide from the latex of Jatropha importation and sequence determination by imensional NMR."; cabaditin is an active peptide which inhibits the pathway of complement activation in vitro. Activity is a syclic peptide. based on an interaction with Cl. is a cyclic peptide. sequencing and scabies. sequencing. based wounds, skins infections and scabies. sequencing.	Score 30.5; DB 1; Length 10; Pred. No. 5.4e+02; 1; Mismatches 1; Indels 1; Gaps
SULT 1 BA_JATMU LABA_JATMU 01-JAN-1990 (Rel. 01-JAN-1990 (Rel. 05-JUL-2004 (Rel. Labaditin. Jatropha multific Eukaryota; viridi Spermatophyta; Ma eurogids 1; Malpi Jatropha. NCBI_TAXID=3996; [1] SEQUENCE. TISSUE=Latex; Kosasi S., van de "Labaditin, a nov multifida L. (Eup means of two-dime FEBS Lett. 256:91 -!- FUNCTION: Lab classical pat seems to be b -!- PTM: This is	Query Match Best Local Similarity 62.5%; Matches 5; Conservative 2 GYWLTIWG 9
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                                          Townsend T., Larson A.;
Townsend T., Larson A.;
"Molecular phylogenetics and mitochondrial genomic evolution in chamaeleonidae (Reptilia, Squamata).";
Mol. Phylogenet. Evol. 23:22-36(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Paton A., Springate D.A., Sudde S., Otieno D., Grayer R., Harlé Willis F., Simonds M.S.J., Powell M.P., Savolainen V.; "Phylogeny and evolution of basils and allies (Ocimeae, Labiata based on three plastid DNA regions."; Mol. Phylogenet. Evol. 31:277-299(2004).

EMBL; AJ505427; CAD45547.1; -. GO: GO:0003735; F:structural constituent of ribosome; IEA. NON TER 1 1 1 NON_TER 8
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Fuerstia africana.
Chloroplast.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; Nepetoideae; Ocimeae; Fuerstia.
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Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases
EMBL; AF448755; AAL90547.1; -.
GO; GO:0005739; C:mitochondrion; IEA.
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                SEQUENCE FROM N.A.
MEDLINE=22169767; PubMed=12182400
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CAD45547;
14-MAR-2004 (TrEMBLrel. 27, Cr
14-MAR-2004 (TrEMBLrel. 27, La
14-MAR-2004 (TrEMBLrel. 27, La
Ribosomal protein (Fragment).
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60.0%;
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NCBI_TaxID=204226;
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05-JUL-2004
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Townsend
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SEQUENCE FROM N.A.

Paton A., Springate D.A., Sudde S., Otieno D., Grayer R., Harley M.M., Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;

"Phylogeny and evolution of basils and allies (Ocimeae, Labiatae) based on three plastid DNA regions.";

Mol. Phylogenet. Evol. 31:277-299(2004).

EMBL; AJ505427; CAD45547.1; -.

Chloroplast; Ribosomal protein.

NON_TER

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NON_TER
                                  Tracheophyta;
dicots; asterids
uerstia.
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Rouimi P., Anglade P., Debrauwer L., Tulliez J.;
Rouimi P., Anglade P., Debrauwer L., Tulliez J.;
"Characterization of pig liver glutathione S-transferases using HPLC-electrospray-ionization mass spectrometry.";
Biochem. J. 317:879-884(1996).
PIR; S71868; S71868.
GO; GO:0004364; F:glutathione transferase activity; IEA.
NON_TER
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Mitochondrion.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Sus.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheog
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
lamiids; Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Fuerstia.
NCBI_TaxID=204226;
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Q7M3E8;
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Glutathione transferase (EC 2.5.1.18) class mu 4 (Fragment)
Sus scrofa domestica (domestic pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleon
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9825;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Cytochrome c oxidase subunit I (Fragment).
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1.8e+06;
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4.8e+03;
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Pred. No.
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Neisseriales;

update) on update)

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SEQUENCE FROM N.A.
STRAIN=MS11;
PubMed=15084227;
Snyder L.A., Davies J.K., Saunders N.J.;
Microarray genomotyping of key experimental strains of Neisserial gonorrhoeae reveals gene complement diversity and five new neisserial genes associated with Minimal Mobile Elements.";
BMC Genomics 5:23-23(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; Strepsirhini; Megaladapidae; Lepilemur
                                                                                                                                                                                                               Saunders N.J.;
EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                            Lepilemur septentrionalis (northern 24 the Eukarnary).
                                                                                                                                                                                                                                                       BACCBB286379D1A6 CRC64;
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MEDLINE=22631663; PubMed=12719521;
Pastorini J., Thalmann U., Martin R.D.;
"A molecular approach to comparative phylogeography
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16C563636B5045B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lemurs.";
Proc. Natl. Acad. Sci. U.S.A. 100:5879-5884(2003)
EMBL; AF224597; AAP33652.1; -.
GO; GO:0005739; C:mitochondrion; IEA.
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Pred. No. 4.8e+03; ; Mismatches 1
                                                            Betaproteobacteria;
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Last sequence up
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STRAIN=MS11;
Snyder L.A.S., Davies J.K., S
Submitted (SEP-2003) to the E
EMBL; AY386266; AAS16521.1; -
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nilarity 60.0%;
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ilarity 57.1%;
Conservative
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1174 MW;
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Bacteria; Proteobacteria;
Neisseriaceae; Neisseria.
NCBI_TaxID=485;
 (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
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Mammalia; Eutheria;
NCBI_TaxID=78584;
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Best Local Similarity
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"Microarray genomotyping of key experimental strains of Neisse:
gonorrhoeae reveals gene complement diversity and five new neigenes associated with Minimal Mobile Elements.";
BMC Genomics 5:23-23(2004).
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                                                                      evolution
Squamata; Iguania; Acrodonta; Chamaeleonidae;
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Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales,
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SEQUENCE FROM N.A.
Townsend T.M., Larson A.L.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases
EMBL; AF448730; AAL90472.1; -.
GO; GO:0005739; C:mitochondrion; IEA.
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                                     SEQUENCE FROM N.A.
MEDLINE=22169767; PubMed=12182400;
Townsend T., Larson A.;
"Molecular phylogenetics and mitochondrial genomic chamaeleonidae (Reptilia, Squamata).";
Mol. Phylogenet. Evol. 23:22-36(2002).
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Pred. No. 4.8e+03;
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4.8e+03;
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Snyder L.A.S., Davies J.K.,
Submitted (SEP-2003) to the
EMBL, AY386266; AAS16521.1;
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          Bradypodion.
NCBI_TaxID=179888;
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05-JUL-2004
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STRAIN=MS11
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NCBI_TaxID=122232;
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SEQUENCE FROM N.A.
GO; GO:0005739; (
Mitochondrion.
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Primates; Strepsirhini; Megaladapidae; Lepilemur
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cheirogaleidae (primates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=22281620; PubMed=12393004;
Pastorini J., Forstner M.R., Martin R.D.;
"Phylogenetic relationships among Lemuridae (Primates): evidence mtDNA.";
J. Hum. Evol. 43:463-478(2002).
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SEQUENCE FROM N.A.
MEDLINE=22631663; PubMed=12719521;
Pastorini J., Thalmann U., Martin R.D.;
"A molecular approach to comparative phylogeography lemurs.";
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SEQUENCE FROM N.A.
MEDLINE=22631663; PubMed=12719521;
Pastorini J., Thalmann U., Martin R.D.;
"A molecular approach to comparative phylogeography
                01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Cytochrome oxidase subunit III (Fragment).
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Last sequence update)
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                                                                             sportive lemur)
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EMBL; AF224595; AAP33644.1; -.
GO; GO:0005739; C:mitochondrion; IEA.
Mitochondrion.
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Proc. Natl. Acad. Sci. U.S.A. 100:5879-5884(2003)
EMBL; AF224641; AAK70615.1; -.
EMBL; AF224642; AAK70619.1; -.
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ed. No. 1.8e+06;
Mismatches 0;
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Pastorini J., Martin R.D., Ehresmann P.,
"Molecular phylogeny of the lemur family
based on mitochondrial DNA sequences.";
Mol. Phylogenet. Evol. 19:45-56(2001).
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Mammalia; Eutheria;
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Cytochrome oxidase subunit III (Fragment).
Name=COIII;
Microcebus ravelobensis.
Microcebus ravelobensis.
Mitochondrion.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Mammalia; Eutheria; Primates; Strepsirhini; Cheirogaleidae;
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Pastorini J., Thalmann U., Martin R.D.;
"A molecular approach to comparative phylogeography
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EMBL; AF224636; AAK70595.1; -.
EMBL; AF224637; AAK70599.1; -.
EMBL; AF224638; AAK70603.1; -.
EMBL; AF224639; AAK70607.1; -.
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MEDLINE=21184272; PubMed=11286490;
Pastorini J., Martin R.D., Ehresmann P.,
"Molecular phylogeny of the lemur family
based on mitochondrial DNA sequences.";
Mol. Phylogenet. Evol. 19:45-56(2001).
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MEDLINE=22631663; PubMed=12719521;
Pastorini J., Thalmann U., Martin R.D.;
"A molecular approach to comparative phylogeography
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MEDLINE=22631663; PubMed=12719521;
Pastorini J., Thalmann U., Martin R.D.;
"A molecular approach to comparative phylogeography
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EMBL; AF224624; AAK70547.1; -.

EMBL; AF224625; AAK70551.1; -.

EMBL; AF224626; AAK70555.1; -.

EMBL; AF224629; AAK70559.1; -.

EMBL; AF224629; AAK70563.1; -.

EMBL; AF224629; C:mitochondrion; IEA.
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                                                                                                   Pastorini J., Martin R.D., Ehresmann P., "Molecular phylogeny of the lemur family based on mitochondrial DNA sequences."; Mol. Phylogenet. Evol. 19:45-56 (2001).
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Pastorini J., Martin R.D., Ehresmann P.,
"Molecular phylogeny of the lemur family
based on mitochondrial DNA sequences.";
Mol. Phylogenet. Evol. 19:45-56(2001).
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MEDLINE=21184272; Pubmed=11286490
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Proc. Natl. Acad. Sci. U.S.A. 100
EMBL; AF224630; AAK70571.1; -.
EMBL; AF224631; AAK70575.1; -.
GO; GO:0005739; C:mitochondrion;
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Name=COIII;
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Eukaryota; Metazoa; C
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NCBI_TaxID=30608;
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Q1-DEC-2001 (TrEMBLrel. 19, Created)
C1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
C1-DEC-2003 (TrEMBLrel. 24, Last annotation update)
CYtochrome c oxidase subunit III (Fragment).
Name=cox3;
Tectocoris diophthalmus (cotton harlequin bug).
Mitochondrion.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;
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MEDLINE=21396409; PubMed=11504862;
Shao R., Campbell N.J., Schmidt E.R., Barker S.C.;
"Increased rate of gene rearrangement in the mitochondrial three orders of hemipteroid insects.";
Mol. Biol. Evol. 18:1828-1832(2001).
EMBL; AF335990; AAK55283.1; -.
GO; GO:0005739; C:mitochondrion; IEA.
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residues 2002273 segs, 358729299 Searched: 2002273 parameters: number of hits satisfying chosen Total

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Database

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1: geneseqp1980s:*

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ALIGNMENTS

Æ 10 standard; peptide; ABP53931 RESULT ABP5393

ABP53931;

entry) (first 09-JAN-2003 ID NO:34 VEGFR-3 binding peptide SEQ

Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3; angiogenesis; lymphangiogenesis; vascular endothelial growth factor; cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic; vulnerary; cell surface receptor; cancer; neovascularisation; liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma; diabetes; PDGF; platelet derived growth factor.

Homo sapiens Synthetic.

Location/Qualifiers "any amino Key Misc-difference

acid" amino "any /note= 10. /note= Misc-difference

acid"

WO200257299-A2

25-JUL-2002

2002WO-IB000099 6-JAN-2002;

2001US-0262476P. 17-JAN-2001; CANCER RES LUDWIG INST C. LICENTIA LTD. (LUDW-) (LICN

Ħ, Kubo வ் Koivunen አ, Alitalo

WPI; 2002-691521/74

activity, useful for y VEGFR-3 ac , , New isolated peptide that inhibits VEGF-C and VEGF-D, diagnosing, evaluating, treating disorders mediated beach as cancer and diseases of neovascularization.

80; 149pp; English Claim 12; Page and The present invention describes an isolated peptide (I) that binds to

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                                                                       of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               emangioma;
inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I) have cytostatic, hepatotropic, antiinflammatory, hypotensive, antidiabetic and vulnerary activities, and can be used in gene therapy. Compositions and methods from the present invention are useful for diagnosing, evaluating and treating disorders mediated by the activity of the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung, liver, spleen, kidney, lymph node, small intestine, blood cells, pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary, skin, head and neck, oesophagus, bone, marrow or blood, and diseases of neovascularisation, e.g. liver diseases, hypertension, post-trauma, chronic hepatitis, haemangiomas and diabetes. The present sequence represents a specifically claimed VEGFR-3 binding peptide from the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3; angiogenesis; lymphangiogenesis; vascular endothelial growth factor; cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic; vulnerary; cell surface receptor; cancer; neovascularisation; liver disease; hypertension; post-trauma; chronic hepatitis; haemangic diabetes; PDGF; platelet derived growth factor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated peptide that inhibits VEGF-C and VEGF-D, useful for diagnosing, evaluating, treating disorders mediated by VEGFR-3 acsuch as cancer and diseases of neovascularization.
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Pred. No. 0.091;
0; Mismatches 0;
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ilarity 100.0%;
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8; Conserv
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                                                                                                                                                                                                         invention
                                                                                                                                                                                                                                        Sequence 10 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to novel isolated polypeptides comprising a sequence that binds an immunoglobulin Fc region. The polypeptides are useful as binding molecules for detecting, isolating or purifying immunoglobulin Fc-region polypeptides present in a solution, e.g. whole blood, plasma or transgenic milk. The Fc-region binding polypeptides are also useful for regulating or preventing an antibody response, or for increasing the half-life and over all stability of a therapeutic or diagnostic compound that is administered to or enters the circulatory system of an individual. This sequence represents an Fc region binding
       pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary skin, head and neck, oesophagus, bone, marrow or blood, and diseases of neovascularisation, e.g. liver diseases, hypertension, post-trauma, chronic hepatitis, haemangiomas and diabetes. The present sequence represents a specifically claimed VEGFR-3 binding peptide from the
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solution,
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purifying immunoglobulin Fc-region polypeptides present
for regulating or preventing an antibody response.
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Pred. No. 0.091;
Mismatches
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Pred. No. 5.2;
1; Mismatches
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                                                                                                                                                                                                                                                                      AAO26093 standard; peptide; 13
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ilarity 100.0%;
Conservative 0
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5; Conservative
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8; Conserv
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                                                                           invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200286070-A2
  spleen,
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                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified
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Matches 5
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design

drug

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GYWCNVWG
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Human serum albumin binding peptide, Seg ID No 297
     standard; peptide; 13
               entry)
              (first
                         Berum
               06-MAY-2004
          ADJ50760;
    ADJ50760
                         human
  ADJ50760
RESULT
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albumin; HSA; serum; blood; tumour; human. WO2003106493-A1 sapiens. Ношо

4-DEC-2003

2003WO-US018896 16-JUN-2003;

2002US-0388642P 14-JUN-2002;

CORP (DYAX-) DYAX Dawson BM; ato AK,

WPI; 2004-082161/08.

separated complex Evaluating sample comprising soluble serum protein by forming compcomprising serum protein and physically associated compounds using peptide ligand that specifically binds with proteins, which is sep evaluated.

297; 191pp; English. SEQ ID NO Disclosure;

compounds. The sample comprises blood or serum, or is obtained from a biopsy. The sample may also be obtained from a tumour or a region within 5 mm of a tumour. The method is useful for detecting modulators that modulate interaction of serum protein-binding compound and serum protein and for identifying binding ligands for serum protein. The present sequence represents a serum albumin-binding peptide identified using the oind to (I) associated iding f the The invention relates to a method of evaluating sample by provisoluble serum protein (I), one or more compounds physically asswith (I), and a (I)-binding agent that comprises a peptide that specifically binds to (I), allowing the (I)-binding agent to bit to form a complex including one or more compounds physically as with (I), separating the complex from one or more components of sample, and evaluating one or more of the physically associated compounds. The sample comprises blood or serum, or is obtained method of the invention

¥. 13 Sequence

Gaps ö Length 13; Indels 2; ω .. Score 43; DB 8 Pred. No. 5.2; 1; Mismatches 79.6%; ilarity 62.5%; Conservative Similarity 5; Conserv Query Match Best Local 3 Best Loc Matches

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8 GYWLTIWG -

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GYWCNVWG

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ABU30004 standard; protein; 474 AA ABU30004; **ABU30004** RESULT П DXTXR

Protein encoded by Prokaryotic essential gene #15531 (first entry) 19-JUN-2003

proliferation; ΑŘ, Ohlsen Forsyth 당, cell Haselbeck R, Yamamoto R, gene; essential ς, β, 2001US-00815242. 2001US-00948993. 2001US-0342923P. 2002US-00072851. 2002US-0362699P. 2002WO-US009107 Malone Carr Antisense; prokaryotic , 30, PHARM 2003-029926/02 B; ACA33874. Zamudio ELITRA WO200277183-A2 06-SEP-2001; 25-OCT-2001; 08-FEB-2002; 06-MAR-2002; Enterococcus 21-MAR-2002; 21-MAR-2001; 03-OCT-2002 Wang L, Wall D, N-PSDB; (ELIT-)

Zyskind JW; Xu HH;

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation of an activity against a biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound; a activity; (11) a culture comprising strains in which the extent to which each of the strains is present in a culture or collection of an organism. The antibions acids are useful for proliferation of an organism. The antisense nucleic acids are useful for the for cellular proliferation to isolate candidate molecules for rational and disponent proprises. screening drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences useful for identifying proteins or screrequired for cellular proliferation to For rational drug discovery programs. English isolate candidate molecules for rational 57928; 1766pp; antisense nucleic acids, homologous nucleic acids SEQ ID NO Claim 25; New for

474 AA; Sequence

Сарв ô Length 474; Indels DB 0, 1.8e+02; Mismatches Score 43; Pred. No. 1 .; 0 79.6%; Conservative Similarity 6; Conserv Query Match Best Local Matches

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-GYWLTIW -1

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ADC97318;

ADC97318

RESULT 6 ADC97318

antibody;

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The present invention provides the protein and coding sequences for the variable regions of human monoclonal antibodies which are immunoreactive with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120. These can be used in diagnosis and therapy of HIV-1 infection
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                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human monoclonal antibody immunoreactive with human immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1 in biological sample and providing passive immunotherapy to HIV-1 infected mammal.
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                                                                                                human monoclonal
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65;
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Mismatches
                                                                antibody SEQ ID NO:
                                                                                               Human immunodeficiency virus-1; HIV-1; lenvelope glycoprotein; gp120; diagnosis
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Pred. No.
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Synthetic.
                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                  30-JUN-1999;
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                                                                Human HIV-1
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                                03-APR-2001
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AAB62747;
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                    Watkins
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AAE093
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated nucleic acid derived from Enterococcus faecium encoding an Enterococcus faecium polypeptide having one of 10 fully defined sequences given in the (or comprising 40 sequential nucleotides chosen from any of the nucleic acids, its complement or sequences hybridising to it). Also included are a recombinant vector comprising the nucleic acid operably linked to transcription regulatory element, a cell comprising the vector and a single-stranded probe comprising the nucleic acid. The nucleic acids is useful for diagnosing pathological conditions resulting from E. faecium bacterial infection (e.g. urinary tract infection) and for screening drugs such as agonists and antagonists. The nucleic acid is useful for recombinant production of Candida albicans derived peptides or antisense polypeptides. Pharmaceutical compositions and vaccines containing the nucleic acid are useful for preventing or treating Enterococcus faecium infections. The present sequence represents one if the disclosed E. faecium proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     isolated nucleic acid derived from Enterococcus faecium encoding prococcus faecium polypeptide useful for detection, prevention and tement of a pathological condition resulting from a bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                   infection; bacteraemia; endocarditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 492;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 43; DB 7; Le
Pred. No. 1.8e+02;
); Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; SEQ ID NO 6945; 243pp; English
                                                                                                                                                   faecium protein sequence SEQ ID 6945
                                                  standard; protein; 492 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                     CORP.
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ilarity 85.7%;
Conservative
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98US-0085598P
                                                                                                                                                                                                                                                                                                                                                                                                                     THERAPEUTICS
                                                                                                                                                                                   Vaccine; urinary tract infe abdominal-pelvic infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bush D;
                                                                                                                     entry)
                                                                                                                                                                                                                                   Enterococcus faecium.
                                                                                                                 (first
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N-PSDB; ADC93664.
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treatment of
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14-MAY-1998;
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Example

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Indels

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23-FEB-2001; 2001WO-US005741

AAB62747 standard; protein; 120 AA.

RESULT 7

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Sequence

Query Match

Local

Best Loc Matches

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112

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Length 120;

4.

30-AUG-2001

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treating Pseudoxanthoma elasticum (PKDS) and PSES associated physiological dysfunctions. The invention is useful for screening for the presence of a PKE mutation. Mutations associated with PKE maps to the ATP-binding cassette transporter ABCC6 (MRP6) gene encodes a 165 kDa protein located in the plasma membrane containing 17 membrane spanning of protein located in the plasma membrane containing 17 membrane spanning contein located in the plasma membrane containing 17 membrane spanning contein located in the plasma membrane domains. PKE is inherited as an autosomal recessive phenotype or appears as a sporadic phenotype. PKE is a heritable disorder characterised by mineralisation of elastic fibers in a heritable disorder characterised by mineralisation of elastic fibers in skin, arterises and the retina, that result in dermal lesions with associated laxity and loss of elasticity, arterial insufficiency, cardiovascular disease and retinal haemorrhages leading to macular degeneration. The method is useful for screening a population of individuals in order to identify individuals with one or more PKE associated MRP6 alleles who are then provided with appropriate genetic counselling in view of the PKE status. The methods are useful for identifying homozygotes, compound heterozygotes or carriers and thus are useful in the area of genetic testing, carrier detection and prenatal diagnosis. The present sequence is human ATP-binding cassette (ABC) truncated mutant which is obtained as the result in the area of genetic testing, carrier detection and prenatal cresult of a stop codon at position 1141 of MRP6 protein. Note: The present sequence is not shown in the specification but is derived from human ATP-binding cassette transporter ABCC6 (MRP6) protein (SED ID NO: ") shown in figure 3 of the specification (ARE09361)
                                                                                                                                                                                                                                                                                                                                                 ng and
siological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chromosome 16;
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                                                                                                                                                                                                                   Screening presence of Pseudoxanthoma elasticum mutation useful for identifying homozygotes, compound heterozygotes or carriers involves determining presence of mutation in MRP6 (ABCC6) nucleic acid.
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                                                                                                                      Terry
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                                                                                                                                                                                                                                                                                                                                               invention relates to methods
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                                                                                                                                                                                                                                                                                                       Claim 10; Page; 163pp; English
                  2000US-0184269P
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larity 71.4%;
Conservative
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                                                                                                                                                           2001-536645/59
B; AAD16258.
                                                          PXE INT INC
                                                                               UNIV HAWAII
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5; Conser
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                  23-FEB-2000;
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                                                        (PXEI-)
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Best Local
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The invention relates to methods and compositions for diagnosing and treating Pseudoxanthoma elasticum (PXE) and PXE associated physiological dysfunctions. The invention is useful for screening for the presence of a dysfunctions. The invention is useful for screening for the presence of a PXE mutation. Mutations associated with PXE maps to the ATP-binding cassette transporter ABCC6 (MRP6-Multidrug Resistance associated protein.)

5) gene locus on chromosome 16. ABCC6 (MRP6) gene encodes a 165 kDa protein located in the plasma membrane containing 17 membrane- spanning helices grouped into three transmembrane domains. PXE is inherited as an autosomal recessive phenotype or appears as a sporadic phenotype. PXE is a heritable disorder characterised by mineralisation of elastic fibers in skin, arterises and the retina, that result in dermal lesions with associated laxity and loss of elasticity, arterial insufficiency, cardiovascular disease and retinal haemorrhages leading to macular degeneration. The method is useful for screening a population of individuals in order to identify individuals with one or more PXE associated MRP6 alleles who are then provided with appropriate genetic counselling in view of the PXE status. The methods are useful for identifying homozygotes, compound heterozygotes or carriers and thus are useful in the area of genetic testing, carrier detection and prenatal diagnosis. The present sequence is mouse AFP-binding cassette (ABC) transporter, ABCC6 (MRP6) protein belonging to sub-family "C". Since ABCC6 protein is involved in drug-resistance it is also called Multidrug CR Resistance associated protein 6 (MRP6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                        Screening presence of Pseudoxanthoma elasticum mutation useful for identifying homozygotes, compound heterozygotes or carriers involves determining presence of mutation in MRP6 (ABCC6) nucleic acid.
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7.7e+02;
                                                                                                                                                                 Terry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 42; DB Pred. No. 7.7e 2; Mismatches
                                                                                                                                                                 7
                                                                                                                                                                                                                                                                                                                                   Example 5; Page 152-159; 163pp; English.
                                                                                                                                                                 Urban
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Misc-difference 1215
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                                                                         2000US-0184269P
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                                                                                                           PXE INT INC.
UNIV HAWAII.
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N-PSDB; AAD16236.
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GYWLSLW
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                                    23-FEB-2001;
                                                                         23-FEB-2000;
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AAY4354
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                                                                                                                                                                                                                                                  The present sequence represents a human MPR-related ABC transporter (MOAT) protein, designated MOAT-E. The protein comprises a multi-domain structure including a tandem repeat of nucleotide binding folds appended C-terminal to a hydrophobic domain, having Walker A and B ATP binding sites and several potential membrane spanning domains. The MOAT nucleic acids are useful for screening a test compound for inhibition of MOAT mediated transport, indicated by restoration of anticancer drug sensitivity, which in turn causes a reduction of transporter mediated cellular efflux of anticancer agents. MOAT DNA or RNA may be used as probes to detect the presence or expression of genes encoding MOAT proteins. Anti-MOAT antibodies are useful for detecting and quantitating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; prenatal diagnosis; dermal lesion; cardiovascular disease; MRP6; Multidrug Resistance-associated protein 6; macular degeneration; ABCC6; ATP-binding cassette transporter; arterial insufficiency; chromosome 16; Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorrhage.
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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== "Nucleotide binding fold-1 (NFB-1) region"
                                                                                                                                                                                                                   anti-cancer drugs
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0
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                                                                                                                                                                                                                   screening for
                                                                                                                                                                                                                                                                                                                                                                                        Score 42;
Pred. No.
                                   TTC"
                                                                                                                                                                                                                                    Claim 39; Page 144-147; 153pp; English.
                                                                                                                                                                        Bain L;
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illarity 71.4%;
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98US-0095153P
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1287
                                    /note=
1455
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N-PSDB; AAZ30081.
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nes 5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATP-binding
                                                                                                                                                      CHASE
                                                                                                                                                                                                                                                                                                                                                                        Sequence 1503 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                      GYWLSLW
                                                                                                                                                                                                                                                                                                                                                                                                                            GYWLTIW
                                                                                                                                                                                                                    New transporter
         Misc-difference
                          Misc-difference
                                             Misc-difference
                                                                                                                                                                       Lee K,
                                                                                                                                                                                                                                                                                                                                                       MOAT proteins
                                                                      WO9949735-A1
                                                                                                          26-MAR-1999;
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03-AUG-1998;
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Best Local
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The invention relates to methods and compositions for diagnosing and treating Pseudoxanthoma elasticum (PXE) and PXE associated physiological dysfunctions. The invention is useful for screening for the presence of a PXE mutation. Mutations associated with PXE maps to the ATP-binding cassette transporter ABCC6 (MRP6, Multidrug Resistance associated protein-c6) gene locus on chromosome 16. ABCC6 (MRP6) gene encodes a 165 kDa protein located in the plasma membrane containing 17 membrane-spanning contains a sportein located into three transmembrane domains. PXE is inherited as an autosomal recessive phenotype or appears as a sporadic phenotype. PXE is a heritable disorder characterised by mineralisation of elastic fibers in skin, arteries and the retina, that result in dermal lesions with associated laxity and loss of elasticity, arterial insufficiency, cardiovascular disease and retinal haemorrhages leading to macular degeneration. The method is useful for screening a population of individuals in order to identify individuals with one or more PXE associated MRP6 alleles who are then provided with appropriate genetic counselling in view of the PXE status. The methods are useful for identifying homozygotes, compound heterozygotes or carriers and thus are useful in the area of genetic testing, carrier detection and prenatal diagnosis. The present sequence is human ATP-binding cassette (ABC) transporter, ABCC6 (MRP6) protein belonging to sub-family "C". Since RBCC6 protein is involved in drug-resistance it is also called Miltidrug
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Pred. No. 7.7e+02;
2; Mismatches 0;
                775. .784
/note= "Nucleotide binding f
1292. .1307
/note= "Nucleotide binding f
1321. .1327
/note= "Nucleotide binding f
1403. .1433
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/note= "Nucleotide binding
"Nucleotide binding
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ilarity 71.4%;
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N-PSDB; AAD16230, A
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AAE09370
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(first entry)
19-NOV-2001
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R1314W (MRP6) transporter ABCC6 cassette Human ATP-binding

mutant

Human; prenatal diagnosis; dermal lesion; cardiovascular disease; MRP6; Multidrug Resistance-associated protein 6; macular degeneration; ABCC6; ATP-binding cassette transporter; arterial insufficiency; chromosome 16; PSP-binding cassette transporter; heritable disorder; retinal haemorrhage; mutant; mutein.

Homo sapiens. Synthetic.

Location/Qualifiers Misc-difference 1314

/note= "Wild type Arg substituted with Trp"

WO200162977-A2

30-AUG-2001

2001WO-US005741. 23-FEB-2001;

2000US-0184269P 23-FEB-2000;

(PXEI-) PXE INT INC (UYHA-) UNIV HAWAII

ß Terry Urban Z, Lesaux O, × Csiszar Boyd CD,

2001-536645/59. B; AAD16263.

N-PSDB;

volves for Screening presence of Pseudoxanthoma elasticum mutation useful identifying homozygotes, compound heterozygotes or carriers indetermining presence of mutation in MRP6 (ABCC6) nucleic acid.

Page; 163pp; English Claim 13;

The invention relates to methods and compositions for diagnosing and treating Pseudoxanthoma elasticum (PXE) and PXE associated physiological dysfunctions. The invention is useful for screening for the presence of a PXE mutation. Mutations associated with PXE maps to the ATP-binding cassette transporter ABCC6 (MRP6-Multidrug Resistance associated protein-cassette transporter ABCC6 (MRP6-Multidrug Resistance associated protein-cassette transmembrane containing 17 membrane-spanning protein located in the plasma membrane containing 17 membrane-spanning autosomal recessive phenotype or appears as a sporadic phenotype. PXE is a heritable disorder characterised by mineralisation of elastic fibers in autosomal recessive phenotype or appears as a sporadic phenotype. PXE is a heritable disorder characterised by mineralisation of elastic fibers in skin, arteries and the retina, that result in dermal lesions with associated laxity and loss of elasticity, arterial insufficiency, cardiovascular disease and retinal haemorrhages leading to macular degeneration. The method is useful for screening a population of individuals in order to identify individuals with appropriate genetic counselling in view of the PXE status. The methods are useful for identifying homozygotes, compound heterozygotes or carriers and thus are useful in the area of genetic testing, carrier detection and prenatal diagnosis. The present sequence is human ATP-binding cassette (ARP6) (MRP6) protein (SED ID NO: 3) shown in the specification but is derived from human ATP-binding cassette transporter ABCC6 (MRP6) protein (SED ID NO: 3) shown in the specification but is derived from human ATP-binding cassette fransporter ABCC6 (MRP6) protein (SED ID NO: 3) shown in the specification but is derived from human ATP-binding cassette fransporter ABCC6 (MRP6) protein (SED ID NO: 3) shown in the specification but is derived from the specification and present sequence is not shown in the specification and present sequence and the sequence and the sequence and the seque

Sequence 1503 AA;

Gaps ö Length 1503; Indels Score 42; DB 4; Li Pred. No. 7.7e+02; 2; Mismatches 0; 77.8%; Conservative Similarity 5; Conserv Query Match Best Local S Matches 5

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971 ~ 965 GYWLSLW GYWLTIW **~**

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RESULT 13

AAE09367 standard; protein; 1503 AA

AAE09367;

entry) (first 19-NOV-2001

mutant. V1298F (MRP6) transporter ABCC6 cassette Human ATP-binding Human; prenatal diagnosis; dermal lesion; cardiovascular disease; MRP6; Multidrug Resistance-associated protein 6; macular degeneration; ABCC6; ATP-binding cassette transporter; arterial insufficiency; chromosome 16, Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorrhage; mutant; mutein

Homo sapiens. Synthetic Location/Qualifiers Misc-difference 1298

substituted with Phe" "Wild type Val /note=

WO200162977-A2

30-AUG-2001

2001WO-US005741 23-FEB-2001;

2000US-0184269P 23-FEB-2000;

PXE INT INC. UNIV HAWAII. (PXEI-) (UYHA-)

Ω, Terry Urban .Z, ò Lesaux Csiszar K, Boyd CD,

2001-536645/59. B; AAD16260. N-PSDB; WPI

Screening presence of Pseudoxanthoma elasticum mutation useful for identifying homozygotes, compound heterozygotes or carriers involves determining presence of mutation in MRP6 (ABCC6) nucleic acid.

Claim 13; Page; 163pp; English.

The invention relates to methods and compositions for diagnosing and treating Pseudoxanthoma elasticum (PXE) and PXE associated physiological dysfunctions. The invention is useful for screening for the presence of a dysfunctions. The invention is useful for screening for the presence of a cassette transporter ABCC6 (MRP6-Multidrug Resistance associated protein.) Gasette transporter ABCC6 (MRP6-Multidrug Resistance associated protein.) For in the plasma membrane containing 17 membrane-spanning helices grouped into three transmembrane domains. PXE is inherited as an autosomal recessive phenotype or appears as a sporadic phenotype. PXE is a heritable disorder characterised by mineralisation of elastic fibers in skin, arteries and the retina, that result in dermal leaions with associated laxity and loss of elasticity, arterial insufficiency, cardiovascular disease and retinal haemorrhages leading to macular degeneration. The method is useful for screening a population of individuals in order to identify individuals with one or more PXE associated MRP6 alleles who are then provided with appropriate genetic counselling in view of the PXE status. The methods are useful for useful in the area of genetic testing, carrier detection and prenatal diagnosis. The present sequence is human ATP-binding cassette (ABC) transporter, ABCC6 (MRP6) V1298F mutant protein. Note: The present sequence is human ATP-binding cassette transporter ABCC6 (MRP6) protein [SED ID NO: 3] shown in final order to identify the sequence is not shown in the specification but is derived from human ATP-final order or sequence is not shown in the specification but is derived in sequence is not shown in the specification but is derived from human ATP-final order or sequence is not shown in the specification but is derived from human ATP-final order or sequence is not shown in the specification but is derived from human ATP-final order to sequence is not shown in the specification to the secure or sequence is sequence. of the specification (AAE09361) m figure

Sequence 1503 AA;

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The invention relates to methods and compositions for diagnosing and treating Pseudoxanthoma elasticum (PXE) and PXE associated physiological dysfunctions. The invention is useful for screening for the presence of a PXE mutation. Mutations associated with PXE maps to the ATP-binding cassette transporter ABCC6 (MRP6-Multidrug Resistance associated protein-containing located in the plasma membrane containing 17 membrane-spanning protein located in the plasma membrane domains. PXE is inheritable disorder characterised by mineralisation of elastic fibers in autosomal recessive phenotype or appears as a sporadic phenotype. PXE is a heritable disorder characterised by mineralisation of elastic fibers in associated laxity and loss of elasticity, arterial insufficiency, cardiovascular disease and retinal haemorrhages leading to macular degeneration. The method is useful for screening a population of individuals in order to identify individuals with one or more PXE associated MRP6 alleles who are then provided with appropriate genetic counselling in view of the PXE status. The methods are useful for identifying homozygotes, compound heterozygotes or carriers and thus are
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55 kDa
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n; ABCC6;
nosome 16;
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                                                                                                                                                                                                                                                                                                 cassette transporter ABCC6 (MRP6) G1302R mutant.
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identifying homozygotes, compound heterozygotes or carriers inv
determining presence of mutation in MRP6 (ABCC6) nucleic acid.
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                                                . 0
                 Score 42; DB 4;
Pred. No. 7.7e+02;
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               77.8%;
illarity 71.4%;
Conservative
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GYWLSLW 971
Query Match
Best Local Similarity
5; Conserv
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N-PSDB; AAD16261.
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; prenatal diagnosis; dermal lesion; cardiovascular disease; MRP6; Multidrug Resistance-associated protein 6; macular degeneration; ABCC6; ATP-binding cassette transporter; arterial insufficiency; chromosome 16; Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorrhage;
                                                     human ATP
                                                                     shown
useful in the area of genetic testing, carrier detection and prenatal diagnosis. The present sequence is human ATP-binding cassette (ABC) transporter, ABCC6 (MRP6) G1302R mutant protein. Note: The present sequence is not shown in the specification but is derived from human binding cassette transporter ABCC6 (MRP6) protein (SED ID NO: 3] show figure 3 of the specification (AAE09361)
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/note= "Wild type A
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UNIV HAWAII
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N-PSDB; AAD16262.
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GYWLSLW
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Matches
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skin, arteries and the retina, that result in dermal lesions with associated laxity and loss of elasticity, arterial insufficiency, cardiovascular disease and retinal haemorrhages leading to macular degeneration. The method is useful for screening a population of individuals in order to identify individuals with one or more PXE associated MRP6 alleles who are then provided with appropriate genetic counselling in view of the PXE status. The methods are useful for identifying homozygotes, compound heterozygotes or carriers and thus are useful in the area of genetic testing, carrier detection and prenatal diagnosis. The present sequence is human ATP-binding cassette (ABC) transporter, ABCC6 (MRP6) Al303P mutant protein. Note: The present sequence is not shown in the specification but is derived from human ATP-binding cassette transporter ABCC6 (MRP6) protein (SED ID NO: 3) shown in n human ATP-3) shown in

Sequence 1503 AA;

Gaps ö Length 1503; Indels Score 42; DB 4; Le Pred. No. 7.7e+02; 2; Mismatches 0; 2 77.8%; Query Match Best Local Similarity 71.4 Matches 5; Conservative

1 GYWLTIW 7 ||||::| 965 GYWLSLW 971 ઠે a

3, 2005, 12:09:53 Search completed: January Job time : 153 secs

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5.1.6
Compugen
version
- 2005
GenCore
(c) 1993
       Copyright
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mode1 8 using protein search, OM protein

12:06:49 2005, e, January Run on:

updat ; Search time 38 Seconds (without alignments) 13.962 Million cell upda

es/sec

SEQ32 54

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BLOSUM62 Gapop 10.0 table Scoring

0.5

Gapext

66318000 residues 478139 segs, Searched

478139 hits satisfying chosen parameters: of number Total

length: length: seq seq DB DB Minimum Maximum

2000000000

100% 45 summaries Post-processing: Minimum Match 0% Maximum Match 10 Listing first 45 Issued_Patents_AA:*
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 /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
 /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
 /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
 /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
 /cgn2_6/ptodata/1/iaa/bcTUS_COMB.pep:*
 /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:* 40m45m Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

		de				
Result						
No.	Score		Length	DB	ID	Description
 	43	79	49	4.	US-09-107-532A-	945, A
7		7	49	4	-09-792-616-9	equence 9, Appl
m			0	4	US-09-792-616-3	quence 3, Appl
4	41	ς.	~	4	-09-071-035-40	equence 408, Ap
S		S.	~	4	-09-134-00	equence 3630, A
9		ù.	9	4	-09-071-035-40	equence 406, Ap
7	40	74.1	668	4	-09-248-796A-193	equence 19350,
8		8	7	4	-107-532A-68	е 6868, А
σ		0	7	4	-09-540-236-2	equence 2629, A
10		œ		4	-09-270-767-4117	equence 41173,
11				4	-270-767-563	equence 56389,
12		ω	3	4	-09-248-796A-227	equence 22785,
13		о Ф	-	4	-09-145-828A-1	equence 11, App
14		ω	~	4	-09-903-4	equence 18, App
15		8	σ	4	-09-252-991A-	equence 23328,
16		8	δ	4	-56	e 18, App
17		8	9	4	-09-221-014-1	equence 18, App
18		8	9	4	-09-252-991A-1	quence 19339,
19		7	Ч	4	-09-252-991A-1913	equence 19134,
20		ف	⊣	~	-318-157	equence 5, Appl
21			Н	4	-09-253-7	equence 5, Appl
22		٠ ن	7	4	-107-532A-6	quence 6560, A
23			Ч	ო	-09-247-373B-	equence 52, App
24			4	~	US-08-512-955-4	e 4, Appl
25			4	4	-252-	e 26736,
56	36	٠. و		7	-08-861-51	, Appl
27			8	-	US-08-414-685-2	equence 2, Appl

Sequence 15188	equence 6, Ap	, Ap	, Ap	equence 6, Ap	equence 6, Ap	equence 2, Ap	equence 2, Ap	equence 4, Ap	Sequence 2, App	equence 4, Ap	equence 2, Ap	equence 4, Ap	, Ap	, Ap	equence 2, Ap	, Ap	AD.
US-09-248-796A-15188	-463-092	2-109A-	US-08-460-907B-6	US-08-463-179A-6	US-08-461-384B-6	US-08-141-893-2	-463-092B-	3-092	A	-462-109A-	0-907B-	US-08-460-907B-4	US-08-463-179A-2	US-08-463-179A-4	US-08-461-384B-2	US-08-461-384B-4	US-08-407-207A-2
367 4	528	528	528	528	528	531	531	531		531	531	531	531	531	1531 3	531	531
9	6.7	6.7	9	6.7	6.7	6.7	6.7	6.7	66.7 1	6.7	6.7	6.7	6.7	6.7	9	6.7	9
36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36
									37								

AT TONMENTO		

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and David Bush
AND AMINO ACID SEQUENCES RELATING TO
FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                              NUMBER OF SEQUENCES: 7310

CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS.CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354

COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: PC
COMPUTER: PC
CORPLIES ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 6945:
SEQUENCE CHARACTERISTICS:
LENGTH: 492 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
LOCATION: (B) LOCATION 1...492
;
SEQUENCE DESCRIPTION: SEQ ID NO: 6945:
US-09-107-532A-6945
RESULT 1
US-09-107-532A-6945
; Sequence 6945, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm all TITLE OF INVENTION: BUTEROCOCCUS FA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enterococcus faecium
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Mon

and Polypeptides

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Sequence 3630, Application US/09134000C

Sequence 3630, Application US/09134000C

Batent No. 6617156

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT FILING DATE: 1998-08-13

PRIOR FILING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SOFTWARE: Patentin version 3.1

SEQ ID NO 3630

LENGTH: 229
                  faecalis Polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    222;
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                                                                 Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 41;
Pred. No.
                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REGISTRATION NUMBER: PB369P2
TELECOMMUNICATION INFORMATION:
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 408:
SEQUENCE CHARACTERISTICS:
LENGTH: 222 amino acids
                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch,
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6
                                                                                                                                                                                                                                                     US/09/071,035
                                                                 me Sciences,
Avenue
Choi
|: Enterococcus
|S: 496
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US-09-134-000C-3630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75.9%;
ilarity 62.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75.9%;
62.5%;
                                                               SEE: Human Genome: 9410 Key West Av
Rockville
 APPLICANT: Gil H. Choi
TITLE OF INVENTION: Ente
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genor
STREET: 9410 Key West
                                                                                                                                                                                                                    SOFTWARE: ASCII Text
CURRENT APPLICATION DATA
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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STRANDEDNESS: si
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Best Local Similarity
Matches 5; Conser
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179 GTWITLWG
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US-09-071-035-408
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US-09-134-000C-3630
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INFORMATION FOR
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                                                                                                            STATE: M
COUNTRY:
ZIP: 208
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Best Local S
Matches 5
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                                                                                                                                                        RESULT 2
US-09-792-616-9
; Sequence 9, Application US/09792616
; Patent No. 6780587
; GENERAL INFORMATION:
; APPLICANT: PXE International, Inc.
; APPLICANT: University of Hawaii
; TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (
; TITLE OF INVENTION: Pseudoxanthoma Elasticum
; FILE REFERENCE: PXE-001
; CURRENT APPLICATION NUMBER: US/09/792,616
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 3
US-09-792-616-3
; Sequence 3, Application US/09792616
; Patent No. 6780587
; GENERAL INFORMATION:
; APPLICANT: University of Hawaii
; TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (
; TITLE OF INVENTION: Pseudoxanthoma Elasticum
; FILE REFERENCE: PXE-001
; CURRENT APPLICATION NUMBER: US/09/792,616
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
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                   492;
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                                                   Indels
                     Length
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red. No. 2.8e+02;
Mismatches 0;
                     4;
                   Score 43; DB Pred. No. 66; 0; Mismatches
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Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 4
US-09-071-035-408
; Sequence 408, Application US/09071035
; Patent No. 6448043
; GENERAL INFORMATION:
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nilarity 71.4%;
Conservative
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illarity 71.4%;
Conservative
                  79.6%;
ilarity 85.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-09-792-616-3
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                                                                                                              112 GYWLTCW 118
                 Query Matcn
Best Local Similarity
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Best Local Similarity
Matches 5; Conser
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Matches 5; Conser
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LENGTH: 1503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       096
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                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 9
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RESULT 8
US-09-107-532A-6868
US-09-107-532A-6868

; Sequence 6868, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; GENERAL INFORMATION:
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                              Gaps
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                                                                                        Length 668;
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                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 71.4%; Score 39; DB 4; Similarity 71.4%; Pred. No. 2.5e+02; 5; Conservative 1; Mismatches 1
                                                                                              DB 4;
2.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: PC
COMPUTER: PC
COMPUTER: PC
COMPUTER: PC
CORTANARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
FILING DATE: 14 May 1998
FILING DATE: 14 May 1998
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REGISTRATION NUMBER: 40,489
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEPHONE: (781)893-8277
                                                                                         DB
                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
LOCATION: (B) LOCATION 1...478
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 6868:
US-09-107-532A-6868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
                                                                                         40;
NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                         Score Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 6868:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
                                                                                        74.1%;
illarity 83.3%;
Conservative
                                       albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||||: |
98 GYWLSAW 104
                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                372 YWMTIW 377
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    ; LENGTH: 668
; TYPE: PRT
; ORGANISM: Candida
US-09-248-796A-19350
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i Sequence 19350, Application US/09248796A

j Patent No. 6747137

i GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 19350
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                                                                                                                                                                                                                            ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
FILING DATE:
CLASSIFICATION:
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Pred. No. 71;
2; Mismatches
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                                                                                                       Sequence 406, Application US/09071035
Patent No. 6448043
GENERAL INFORMATION:
APPLICANT: Gil H. Choi
TITLE OF INVENTION: Enterococcus
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB36
TELEPHONE: (301) 309-8504
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 406:
SEQUENCE CHARACTERISTICS:
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ilarity 62.5%;
Conservative
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amino acid
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203 GTWITLWG 210
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203 GTWITLWG 210
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MLECULE TYPE: pro171-035-406
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Best Local Similarity
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  Score 37; DB Pred. No. 26; 3; Mismatches
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APPLICANT: Kirchner, Stephen J.
APPLICANT: Firchner, Stephen J.
APPLICANT: Parker-Barnes, Jennifer M.
TITLE OF INVENTION: THE ELONGASE GENE AND US
FILE REFERENCE: 6407.US.Ol
CURRENT APPLICATION NUMBER: US/09/145,828A
CURRENT FILING DATE: 1998-09-02
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
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Mukerji, Pradip
Leonard, Amanda E. Y
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Thurmond, Jennifer
Kirchner, Stephen J
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Conservative
68.5%;
illarity 57.1%;
Conservative
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100.0%;
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OTHER INFORMATION: Identity
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SEQ ID NO 22785
LENGTH: 132
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Best Local Similarity
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Query Match
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16 HWLSLWG
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                                                               YWLTIWG
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US-09-248-796A-22785
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US-09-145-828A-11
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LENGTH: 278
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FEATURE:
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APPLICANT:
APPLICANT:
APPLICANT:
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Sequence ...
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 41173
LENGTH: 24
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                                           Sequence 2629, Application US/09540236

Patent No. 6673910

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2005-001

CURRENT APPLICATION NUMBER: US/09/540,236

CURRENT FILING DATE: 2000-04-04

NUMBER OF SEQ ID NOS: 3840

SEQ ID NO 2629

LENGTH: 328
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Sequence 56389, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:

TITLE OF INVENTION: Nucleic acids and proteins of Droteine OF INVENTION: Nucleic acids and proteins of Droteine OF INVENTION: Nucleic acids and proteins of Droteine OF INVENTION: Number: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 56389
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Pred. No.
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Pred. No.
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US-09-270-767-56389
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ilarity 71.4%;
Conservative
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57.1%;
vative
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US-09-540-236-2629
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16 HWLSLWG
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TYPE: PF
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US-09-248796A-22785

i Sequence 22785, Application US/09248796A

j Patent No. 6747137

j GENERAL INFORMATION:

i APPLICANT: Keith Weinstock et al

i TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS

j TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

j TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

j TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

j FILE REFERENCE: 107196.132

j CURRENT APPLICATION NUMBER: US 60/074,725

j PRIOR FILING DATE: 1998-02-13

j PRIOR FILING DATE: 1998-08-13

j PRIOR FILING DATE: 1998-08-13

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Pred. No. 1.4e+02,
); Mismatches 0,
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Pred. No. 2.8e+02;
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FENTION: THE ELONGASE GENE AND USES
ICE: 6407.US.01
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US-09-252-991A-23328
; Sequence 23328, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING;
; TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
; TITLE OF INVENTION: APPLICATION NUMBER: US/09/252,991A
; CURRENT APPLICATION NUMBER: US 60/074,788
; PRIOR PILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23328
; LENGTH: 499
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                                                                   RESULT 14
US-09-903-456-18

JS-quence 18, Application US/09903456

Patent No. 6677145

GENERAL INFORMATION:

APPLICANT: Abbott Laboratories

APPLICANT: Huang, Yung-Sheng

CURRENT HILD OF INVENTION: ELONGASE GENES AND USES THEREOF

FILE REFERENCE: 6407.US.P3

CURRENT FILING DATE: 2001-07-11

PRIOR APPLICATION NUMBER: US 09/624,670

PRIOR APPLICATION NUMBER: US 09/379,095

PRIOR APPLICATION NUMBER: US 09/145,828

PRIOR FILING DATE: 1999-08-23

PRIOR FILING DATE: 1998-09-02

NUMBER OF SEQ ID NOS: 116

SOFTWARE: FABELSEQ for Windows Version 4.0
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Pred. No. 2.8e+02;
2; Mismatches 1;
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Pred. No. 5e+02;
2; Mismatches
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Best Local Similarity 57.1%;
Matches 4; Conservative
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llarity 57.1%;
Conservative
|||::|
108 GYWIFLW 114
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US-09-252-991A-23328
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GYWISAW 117
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108 GYWIFLW 114
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Best Local Similarity
Matches 4; Conser
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SEQ ID NO 18
LENGTH: 278
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Scoring table

, Gapext 0.5 BLOSUM62 Gapop 10.0 residues 1599051 seqs, 359727711 Searched: 599051 of hits satisfying chosen parameters: Total number

length: 0 length: 2000000000 sed sed DB DB Minimum Maximum

summaries 100% 45 81 Post-processing: Minimum Match 08 Maximum Match 10 Listing first 45 Maximum Listing Database

Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*

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10: /cgn2_6/ptodata/2/pubpaa/USO96_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/USO96_PUBCOMB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/USO90_NEW_PUB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/USO08_PEP:*

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16: /cgn2_6/ptodata/2/pubpaa/USO08_PEP:*

17: /cgn2_6/ptodata/2/pubpaa/USO08_PEP:*

18: /cgn2_6/ptodata/2/pubpaa/USO08_PEP:*

19: /cgn2_6/ptodata/2/pubpaa/USO08_PEP:*

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SUMMARIES

		Description	nc	Sequence 35, Appl	73,	Sequence 297, App	5792		ο,	6	Sequence 3, Appli	'n	114,	Sequence 338, App	43458,
		QI	10-046-	US-10-046-922-35	US-10-125-869A-73	US-10-462-262-297	US-10-282-122A-57928	US-10-437-963-190740	US-09-792-616-9	US-10-764-328-9	US-09-792-616-3	US-10-764-328-3	US-10-125-869A-114	US-10-462-262-338	US-09-864-761-43458
		DB	13	13	14	15	15	16	10	16	10	16	14	15	σ
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Sequence 24089, A Sequence 406, A Sequence 406, A Sequence 19, Ap Sequence 17, A Sequence 21, A Sequence 21, A Sequence 23, A Sequence 37, A Sequence 37, A Sequence 41, A Sequence 86, A Sequence 299, A Sequence 299, A Sequence 299, A Sequence 299, A Sequence 22681	Sequence 5178, Ap Sequence 88, Appl Sequence 52805, A Sequence 57680, A Sequence 4579, Ap Sequence 260407,
S-10-424-599-24 -09-071-035-408 S-10-206-576-40 S-10-206-576-40 S-10-206-576-40 S-10-206-576-40 S-10-206-576-40 S-10-206-576-40 S-10-424-599-19 S-09-910-483-13 S-09-910-483-13 S-09-910-483-25 S-09-910-483-33 S-09-910-483-33 S-09-910-483-33 S-09-910-483-33 S-09-910-483-33 S-09-910-483-33 S-10-160-232-86 S-10-160-232-86 S-10-160-232-86 S-10-424-599-22 S-10-425-115-18	US-09-738-626-5178 US-10-091-007-88 US-10-282-122A-52805 US-10-282-122A-57680 US-09-738-626-4579 US-10-425-115-260407
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ALIGNMENTS

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                                Sequence 34, Application US/10046922

Sequence 34, Application US/10046922

GENERAL INFORMATION:

APPLICANT: Alitalo, Kari

APPLICANT: Kubo, Hajime

TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS

FILE REFERENCE: 28967/37084A

CURRENT APPLICATION NUMBER: US/10/046,922

CURRENT FILING DATE: 2002-01-15

NUMBER OF SEQ ID NOS: 80

SOFTWARE: Patentin version 3.0

SEQ ID NO 34

LENGTH: 10
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100.0%; Pred. No. 0.22;
tive 0; Mismatches 0.
                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: isolated peptide
FEATURE:
NAME/KEY: SITE
LOCATION: (1)..(1)
OTHER INFORMATION: X is any amino acid
NAME/KEY: SITE
LOCATION: (10)..(10)
OTHER INFORMATION: X is any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                      is any amino acid
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Best Local Similarity
Matches 8; Conser
RESULT 1
US-10-046-922-34
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SOFTWARE: PatentIn ver
SEQ ID NO 57928
LENGTH: 474
                                                                                                                                            TYPE: PRT
ORGANISM: Artificial
FEATURE:
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US-10-462-262-297
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TYPE: PRT
ORGANISM:
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Best Local S
Matches 5
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APPLICANT:
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                                                                                                                 INHIBITOR MATERIALS AND METHODS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Ley, Arthur C.
APPLICANT: Stochl, Mark
APPLICANT: Ransohoff, Thomas C.
APPLICANT: Potter, M. Daniel (deceased)
TITLE OF INVENTION: BINDING MOLECULES FOR FC-REGION
TITLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 3421.1006-001
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                                                                                                                                                                                                                                                                                                        Score 54; DB 1. Pred. No. 0.22;
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                                                                                                                                                                                                                                                                                                                                        Mismatches
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Mismatches
US-10-046-922-35
; Sequence 35, Application US/10046922
; Publication No. US20020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Kubo, Hajime
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERI
; FILE REFERENCE: 28967/37084A
; CURRENT APPLICATION NUMBER: US/10/046,922
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/125,869A CURRENT FILING DATE: 2002-11-19
PRIOR APPLICATION NUMBER: 60/284,534
PRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 200
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 43;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 73, Application US/10125869A
Publication No. US20030199671A1
GENERAL INFORMATION:
APPLICANT: Rondon, Isaac Jesus
APPLICANT: Wu, Qi-Long
APPLICANT: Ley, Arthur C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-462-262-297
; Sequence 297, Application US/10462262
; Publication No. US20040009534A1
; GENERAL INFORMATION:
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US-10-046-922-35
                                                                                                                                                                                                                                                                                                                         Similarity 100
8; Conservative
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Dawson, Bruce
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US-10-125-869A-73
                                                                                                                                                                                                             SEQ ID NO 35
LENGTH: 10
TYPE: PRT
ORGANISM: i
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ENGTH: 13
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Matches 5
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Best Local
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APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yanamoto, Robert
APPLICANT: Yanamoto, Robert
APPLICANT: You, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPERDER.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
CURRENT APPLICATION NUMBER: 06/10/2020
PRIOR PILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-10-23
PRIOR PELING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/250,931
PRIOR APPLICATION NUMBER: 60/250,938
PRIOR APPLICATION NUMBER: 60/250,938
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/250,938
PRIOR PILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: immunoglobulin binding polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 43; DB 15;
Pred. No. 10;
1; Mismatches
FILE REFERENCE: 10280-052001
CURRENT APPLICATION NUMBER: US/10/462,262
CURRENT FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: US 60/388,642
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 430
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 297
LENGTH: 13
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Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 78614
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US-10-282-122A-57928
; Sequence 57928, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
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ilarity 62.5%;
Conservative
                                                                                                                                                                                                                                                                                                                            Sequence
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Malone, Cheryl
Haselbeck, Robert
Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Sequence 3, Application US/10764328

Publication No. US20040166521A1

GENERAL INFORMATION:
APPLICANT: PXE International, Inc.
TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter;
TITLE OF INVENTION: Pseudoxanthoma Elasticum
FILE REFERENCE: PXE-001PC
CURRENT APPLICATION NUMBER: US/10/764,328

CURRENT FILING DATE: 2004-01-23
                                                                                                                                                                     transporter
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                                                                             Sequence 9, Application US/10764328
; Publication No. US20040166521A1
; GENERAL INFORMATION:
; APPLICANT: PXE International, Inc.
; APPLICANT: University of Hawaii
; TITLE OF INVENTION: Mutations in a gene encoding an TITLE OF INVENTION: Pseudoxanthoma Elasticum; FILE REFERENCE: PXE-001PC
; CURRENT APPLICATION NUMBER: US/10/764,328
; CURRENT FILING DATE: 2004-01-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 1498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ore 42; DB 10; 3d. No. 9.3e+02; Mismatches 0;
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Pred. No. 9.3e+02;
Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: PXE International, Inc.
APPLICANT: University of Hawaii
ITILE OF INVENTION: Mutations in a gene encoding
TITLE OF INVENTION: Pseudoxanthoma Elasticum
FILE REFERENCE: PXE-001
CURRENT APPLICATION NUMBER: US/09/792,616
CURRENT FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.0
SEQ ID NO 3
LENGTH: 1503
TYPE: PRT
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                     Mus musculus
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US-09-792-616-3
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   990 GYWLSLW 966
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965 GYWLSLW 971
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: NUMBER: US/10/437,963
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
LENGTH: 671
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Publication No. US20030165828A1
GENERAL INFORMATION:
APPLICANT: PXE International, Inc.
APPLICANT: University of Hawaii
TITLE OF INVENTION: Mutations in a gene encoding an ABC transport
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US-10-437-963-190740
                               Score 43; DB 15;
Pred. No. 2.4e+02;
); Mismatches 1;
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Pred. No. 3.3e+02;
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Pred. No. 9.3e+02;
2; Mismatches (
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CURRENT APPLICATION NUMBER: US/09/792,616
CURRENT FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.0
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US-10-437-963-190740
; Sequence 190740, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
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nilarity 85.7%;
Conservative
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illarity 71.4%;
Conservative
                            79.6%;
                                               Local Similarity 85.7
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APPLICANT: Wu, Qi-Long
APPLICANT: Stochl, Mark
APPLICANT: Stochl, Mark
APPLICANT: Ransohoff, Thomas C.
APPLICANT: Ransohoff, Thomas C.
APPLICANT: Potter, M. Daniel (deceased)
TITLE OF INVENTION: BINDING MOLECULES FOR FC-REGION
TITLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 3421.1006-001
CURRENT APPLICATION NUMBER: US/10/125,869A
CURRENT FILING DATE: 2002-11-19
PRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 200
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 114
LENGTH: 14
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ced. No. 9.3e+02;
Mismatches 0
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CTHER INFORMATION: Fc region binding polypeptide US-10-125-869A-114
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Mismatches
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Publication No. US20040009534A1;
GENERAL INFORMATION:
APPLICANT: Sato, Aaron K.
APPLICANT: Dawson, Bruce M.
TITLE OF INVENTION: PROTEIN ANALYSIS
FILE REFERENCE: 10280-052001
CURRENT APPLICATION NUMBER: US/10/462,262
CURRENT APPLICATION NUMBER: US 60/388,642;
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 430
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 338
LENGTH: 14
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Pred. No. 21
                                                                                                                          Score 42;
Pred. No. 9
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Publication No. US20030199671A1
GENERAL INFORMATION:
APPLICANT: Rondon, Isaac Jesus
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nilarity 71.4%;
Conservative
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Wu, Qi-Long
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llarity 62.5%;
Conservative
               version 3
                                                                          ; ORGANISM: Homo sapiens
US-10-764-328-3
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965 GYWLSLW 971
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ORGANISM: Artificial
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US-10-125-869A-114
SOFTWARE: Pater
SEQ ID NO 3
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APPLICANY: Rank, David R.
APPLICANY: Rank, David R.
APPLICANY: Rank, David R.
APPLICANY: Chen, Wensheng
TITLE OF INVENTION: GENB EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT APPLICATION NUMBER: US 66/140,312
PRIOR PLING DATE: 2001-05-26
PRIOR PLING DATE: 2000-06-23
PRIOR PLING DATE: 2000-10-49
PRIOR PLING DATE: 2000-10-49
PRIOR PLING DATE: 2000-10-49
PRIOR PLING DATE: 2001-01-30
PRIOR PRIOR PLING WIMBER: PCT/US01/0663
PRIOR PLING DATE: 2001-01-30
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; FEATURE:
; OTHER INFORMATION: immunoglobulin binding polypeptide
US-10-462-262-338
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Sequence Listing Engine
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NUMBER
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INFORMATION: EXPRESSED IN LUNG, 8
INFORMATION: EXPRESSED IN BRAIN,
                                                                                                                                                                                                                                                                                                                                                                             Sequence 43458
Sequence 43458, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US (PRIOR FILING DATE: 2001-01-29 NUMBER OF SEQ ID NOS: 49117 SOFTWARE: Annomax Sequence Lie
                                                                                                            75.9%;
62.5%;
                                                                                                                                    Similarity 62.
5; Conservative
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US-10-424-599-240891
; Sequence 240891, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: La Rosa Thomas J
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: 18-21(53223) B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 240891
; LENGTH: 82
; TYPE: PRT
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IN BONE MARROW, SIGNAL
IN PLACENTA, SIGNAL = 1
IN FETAL LIVER, SIGNAL
IN ADULT LIVER, SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
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Pred. No. 1e+02;
1; Mismatches
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                                                                               Score 41; DB :
Pred. No. 46;
3; Mismatches
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ET: 9410 Key West Avenue
: Rockville
E: Maryland
TRY: USA
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larity 62.5%;
Conservative
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CURRENT APPLICATION DATA
APPLICATION NUMBER: U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: un
FEATURE:
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OTHER INFORMATION: E OTHER INFORMATION: E OTHER INFORMATION: E OTHER INFORMATION: E S-09-864-761-43458
                                                                             Query Match
Best Local Similarity
Matches 5; Conser
                                                                                                                                   1 GYWLTIWG
|||:|::|
25 GYWITVFG
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hes 5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: US-10-424-599-240891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GYWLTIW
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NAME/KEY: unsure
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STATE: M
COUNTRY:
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5.1.6 Compugen Ltd version - 2005 GenCore (c) 1993 Copyright

sw model using - protein search, OM protein

/ Search time 38 Seconds
(without alignments)
20.256 Million cell updates/sec 2005, 12:03:34 3, January Run on:

SEQ32 54 score: Title: Perfect

gywltiwg ~ Sequence:

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Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

of hits satisfying chosen parameters: Total number

283416 seqs, 96216763 residues

Searched:

283416

DB DB

length: 0 length: 2000000000 sed sed Minimum Maximum

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* 1 2 E 4

. No. is the number of results predicted by chance to have a e greater than or equal to the score of the result being printed, is derived by analysis of the total score distribution. Pred. N score g and is

		de			SUMMARIES	
	Score	Query	Length	DB		scription
, ₋₁	42		441	. 0	9530	probable transport
7	42		0	7	4221	idrug resista
m	41		\mathbf{a}	7	C411	plication prot
4,	41	75.9	419	7	E90446	[import
ហ	40		T	~	3490	chain p
φ	40		\sim	~	7103	Na+/H+-
7	40	74.1		~	9528	probable ABC trans
6 0	39	72.2		~	F197	cal pr
σ	99	72.2	~	~	4674	orn'
10	39	72.2	$\mathbf{\sigma}$	~	8687	/ornitin
11	38	0	_	~	3573	inte
12	38	0	\sim	~	7517	iporte
13	38	70.4	\sim	~	9025	orter [
14	38	0	m	~	5010	oxidor
15	38	70.4	\sim	~	5888	d buipt
16	C	Q	\sim	~	7184	ding
17	37.5	Ø	10	~	3383	lux
18	7.	69.4	90	~	C470	inc,
19	37	68.5	\sim	Н	VMS1	shain
20	37	68.5	10	~	F088	probable exported
21	37	68.5	_	7	1223	hypothetical prote
22	37	68.5	m	Н	1386	Ö
23	37	68.5		~	F235	al
24	37	68.5	_	~	7638	netical
25	37	68.5	286	~	8869	F41H10.
26	37	68.5	\mathbf{a}	~	4916	Lysk-type protein
27	37	ъ Э	10	~	7475	lucos
28	37	68.5	m	7	1283	heavy cha
29	37	а Э	_	~	F112	od shape-determ

RESULT 2
T42216
multidrug resistance-associated protein homolog MLP-1 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T42216
C;Accession: T42216
R;Hirohashi, T.; Suzuki, H.; Ito, K.; Ogawa, K.; Kume, K.; Shimizu, T.; Sugiyama, Y.
Mol. Pharmacol. 53, 1068-1075, 1998
A;Title: Hepatic expression of multidrug resistance-associated protein-like proteins mai
A;Title: Hepatic expression of multidrug resistance-associated protein-like proteins mai
A;Reference number: Z22081; MUID:98279126; PMID:9614210
A;Accession: T42216
A;Status: preliminary; translated from GB/EMBL/DDBJ

robable amino ac	inine/ornithi	nine/	probable transcarb	othetical	sphatidylg <u>ī</u> y	tial probab	othetical prot	cyl-sn-glycero	cylglycerol-3-	the	protein - ye	etical prot	hypothetical prote	protein - y	ıble membran
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~	482	σ	0	9	7	3	4	4	4	S	œ	σ	S	B	38
8.5 47	5 48	8.5 49	7.6 60	6.7 16	6.7 17	6.7 23	6.7 24	6.7 24	6.7 24	6.7 25	6.7 28	6.7 29	6.7 35	6.7 38	6.7 3
7 68.5 47	8.5 48	7 68.5 49	5 67.6 60	6 66.7 16	6 66.7 17	6 66.7 23	6 66.7 24	6 66.7 24	6 66.7 24	6 66.7 25	6 66.7 28	6 66.7 29	6 66.7 35	6 66.7 38	6 66.7 3

ALIGNMENTS

	RESULT 1	
	probable transport protein SMa0684 [imported] - Sinorhizobium meliloti (strain 1021)	loti (strain 1021) mag
	C; Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004	-Jul-2004
	C; Accession: C95307 R; Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barlo	arlov-Hubler, F.; Bows
	.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh,	
	Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001 A:Title: Nicleotide semience and predicted functions of the entire Sin	Sinorbizobium melilor
	A; Reference number: A95262; MUID: 21396509; PMID:11481432	
	A; Accession: C95307 A; Status: preliminary	
	A; Molecule type: DNA	
	A; Cross-references: UNIPROT: Q92ZT6; GB: AE006469; PIDN: AAK65021.1; PID:	PID:q14523451; GSPDB:G
	A; Experimental source: strain 1021, megaplasmid pSymA	
	R; Galibert, F; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe,	pe, F.; Barloy-Hubler,
	pela, D.; Chain, P.; Cowle, A.; Davis, R.W.; Dreano, S.; Federspiel, N	l, N.A.; Fisher, R.F.;
	L.; Hyman, K.W.; Jones, I. Science 293, 668-672, 2001	
	A; Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.;	E.; Komp, C.; Lelaure,
	hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.;	.H.; Wong, K.; Yeh, K.
	A; Title: The composite genome of the legume symbiont Sinorhizobium meliloti. A: Reference number: A96039: MITD:21368234: DMTD:11474104	meliloti.
	A; Contents: annotation	
	C;Genetics:	
	A;Gene: Smauck4 A;Genome: plasmid	
	C;Superfamily: L-lysine transport protein	
	Query Match 77.8%; Score 42; DB 2; Length 441;	
	vative 2; Mismatches 0; Indels 0;	; Сарв 0;
	Oy 1 GYWLTIW 7	
	Db 92 GYWISIW 98	

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Best Local Similarity
Matches 6; Conser
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A;Molecule type: mRNA
A;Residues: 1-1502 <HIR>
A;Cross-references: UNIPROT:088269; EMBL:AB010466; NID:g3242457; PIDN:BAA28954.1; PID:g3
A;Experimental source: strain Sprague-Dawley; liver
C;Superfamily: human multidrug resistance protein cMOAT2; ATP-binding cassette homology
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Joc, H.P.; Redder
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C; Species: Sulfolobus solfataricus
C; Species: Sulfolobus solfataricus
C; Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul
C; Accession: E90446
R; She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Av
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngon
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A; Description: Sulfolobus solfataricus complete genome.
A; Reference number: A99139
A; Accession: E90446
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-419 < KUR>
A; Residues: 1-419 < KUR>
A; Genetics:
C; Genetics:
A; Genetics:
                                                                                                                                                                                                                                                                                                 replication protein homolog - Pyrococcus sp. (fragment)
N;Alternate names: hypothetical 391 protein
C;Species: Pyrococcus sp.
C;Date: 07-Feb-1996 #sequence_revision 19-Apr-1996 #text_change 17-M
C;Accession: PC4117
R;Rashid, N.; Morikawa, M.; Imanaka, T.
Gene 166, 139-143, 1995
A;Title: An abnormally acidic TATA-binding protein from a hypertherm A;Reference number: JC4514; MUID:96105215; PMID:8529878
A;Accession: PC4117
A;Molecule type: DNA
A;Residues: 1-391 <RAS>
A;Cross-references: DDBJ:D50018
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2; Mismatches
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Pred. No. 43;
2; Mismatches
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Mismatches
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Pred. No. 4
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Ig heavy chain precursor V region (5-27)
C;Species: Mus musculus (house mouse)
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Best Local Similarity 71.4%;
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probable ABC transporter, periplasmic solute-binding protein, family 5 SMa0302 [imported] c; Species: Sinorhizobium meliloti
C; Species: Sinorhizobium meliloti
C; Species: Sinorhizobium meliloti
C; Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C; Accession: C95282
R; Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowse.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.; Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A; Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti A; Reference number: A95262; MUID:21396509; PMID:11481432
A; Reference number: A95262; MUID:21396509; PMID:11481432
A; Accession: C95282
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-508 <KUR>
A; Cross-references: UNIPROT:0930N2; GB:AE006469; PIDN:AAK64821.1; PID:g14523232; GSPDB:GR
A; Residuental source: strain 1021, megaplasmid pSymA
A; Ralibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, Pela, Hyman, R.W.; Jones, T.
L.; Hyman, R.W.; Jones, T.
                                                                                                                                          cross-read
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J.; Kushida,
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C;Species: Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Ji
C;Accession: B71038
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.;
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.;
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a language in B71038
A;Title: Complete sequence and gene organization of the genome of a language in B71038
A;Accession: B71038
A;Accession: B71038
A;Accession: B71038
A;Katus: preliminary; nucleic acid sequence not shown; translation almost in B71038
A;Residues: 1-425 < KAW>
A;Residues: 1-425 < KAW>
A;Cross-references: UNIPROT:059255; GB:AP000006; NID:g3236133; PIDN:1A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence c;Genetics:
A;Gene: PH1594
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C; Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 16-C; Accession: C34903
R; Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
J. Biol. Chem. 265, 133-138, 1990
A; Title: Active site structure and antigen binding properties of id A; Reference number: A34903; MUID: 90094387; PMID: 2104617
A; Accession: C34903
A; Status: preliminary; not compared with conceptual translation A; Molecule type: mRNA
A; Residues: 1-142 < BED>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 34-119/Domain: immunoglobulin homology < IMM>
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Mismatches
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Best Local Similarity 62.5%;
Matches 5; Conservative
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51 FWLSLWG 57
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Best Local Similarity
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                     C.; Lelaure,
, K.; Yeh, K.
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Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ID:g17130724; GSPDB:G
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                        3.; Komp, C
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09-Jul-2004
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C; Species: Lactobacillus sakei
C; Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-C; Accession: T46745
C; Accession: T46745
R; Zuniga, M.; Champomier-Verges, M.C.; Perez-Martinez, G.; Zagorec, M.; J. Bacteriol. 180, 4154-4159, 1998
A; Title: Structural and functional analysis of the gene cluster encodin A; Reference number: Z23141; MUID:98361904; PMID:9696763
A; Accession: T46745
A; Accession: T46745
A; Molecule type: DNA
A; Residues: 1-475 < ZUN>
A; Cross-references: UNIPROT:053092; EMBL:AJ001330; NID:g2764610; PIDN:C
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Science 293, 668-672, 2001
A; Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.A; Title: The composite genome of the legume symbiont Sinorhizobium A; Reference number: A96039; MUID:21368234; PMID:11474104
A; Contents: annotation
C; Genetics:
A; Gene: SMa0302
A; Genome: plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accessions preliminary
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-376 < KUR>
A; Cross-references: UNIPROT: Q8YX40; GB: BA000019; PIDN: BAB73334.1;
                                                                                                                                                                                                                                                                                                                                                                          (strain PCC
                                                                                                                                                                                                                                                                                                                                                                                    C; Species: Nostoc sp. PCC 7120
A; Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp.
C; Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change
C; Accession: AF1978
R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S. Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, N
                                                                                                                                                                              Length 508;
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Pred. No. 74;
0; Mismatches
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Pred. No. 79;
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A; Pathway: arginine catabolism
C; Superfamily: L-lysine transport
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C;Genetics:
A;Gene: arcD
C;Function:
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actions of the antiporter [imported] - Lactococcus lactis subsp. lactis (strain IL140 C; Species: Lactococcus lactis subsp. lactis C; Species: Lactococcus lactis subsp. lactis C; Species: Lactococcus lactis subsp. lactis C; Date: 23-Mar-2001 #text_change 09-Jul-2004 C; Date: 23-Mar-2001 #text_change 09-Jul-2004 C; Accession: C86879 C; Accession: C86879 C; Accession: C86879 A; Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss A; Reference number: A86625; MUID:21235186; PMID:11337471 A; Reference number: A86625; MUID:11337471 A; Reference number: A86625; 
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C75176
na+/h+ antiporter (napa-2) PAB0390 - Pyrococcus abyssi (strain Orsay)
C; Species: Pyrococcus abyssi
C; Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C; Accession: C75176
R; anonymous, Genoscope
R; anonymous, Genoscope
Submitted to the EMBL Data Library, July 1999
A; Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B.G.; Rajandream,
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C; Species: Streptomyces coelicolor
C; Species: Streptomyces coelicolor
C; Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C; Accession: T35739
R; Saunders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajance submitted to the EMBL Data Library, August 1999
A; Reference number: Z21588
A; Accession: T35739
A; Reference number: Z21588
A; Accession: T35739
A; Staus: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-118 <SAU>
A; Cross-references: UNIPROT: Q9S2K9; EMBL: AL109732; PIDN: CAB52050.1; GSPDB: GN0007
A; Experimental source: strain A3(2)
C; Genetics:
A; Gene: SCOEDB: SC7H2.08
C; Superfamily: Streptomyces coelicolor probable integral membrane protein SC7H2.
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1e+02;
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nilarity 71.4%;
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Best Local Similarity 57.1%;
Matches 4; Conservative
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A; Reference number: A75001
A; Accession: C75176
A; Accession: C75176
A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-426 <KAW>
A; Residues: 1-426 <KAW>
A; Experimental source: strain Orsay
C; Genetics:
A; Genetics:
A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABCTransporter [imported] - Sulfolobus solfataricus
C; Species: Sulfolobus solfataricus
C; Species: Sulfolobus solfataricus
C; Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C; Accession: G90251
R; She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Ch Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
Submitted to GenBank, April 2001
A; Description: Sulfolobus solfataricus complete genome.
A; Reference number: A99139
A; Accession: G90251
A; Residues: preliminary
A; Residues: 1-477 < KUR>
A; Residues: 1-477 < KUR>
A; Residues: 1-477 < KUR>
A; Genetics:
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C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
C;Accession: T50103
R;Seeger, K.; Harris, D.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
Submitted to the EMBL Data Library, January 2000
A;Reference number: Z25038
A;Accession: T50103
A;Reference number: Z25038
A;Accession: T50103
A;Accession: T50103
A;Accession: T50103
A;Cross-references: UNIPROT:Q9US28; EMBL:AL136499; PIDN:CAB66164.1; GSPDB:GN0006
A;Experimental source: strain 972h(-); cosmid c1783
C;Genetics:
A;Gene: SPDB:SPAC1783.01
A;Map position: 1
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GSPDB:GN00066; SPDB

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Ins P4-binding protein - human

C;Species: Homo sapiens (man)

C;Species: Homo sapiens (man)

C;Species: Homo sapiens (man)

C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 04-Apr-2004

C;Accession: S58888

R;Cullen, P.J.; Hsuan, J.J.; Truong, O.; Letcher, A.J.; Jackson, T.R.; Dawson, A.P.; Irvanature 376, 527-530, 1995

A;Title: Identification of a specific Ins(1,3,4,5)P(4)-binding protein as a member of the A;Reterence number: S58888; MUID:95364929; PMID:7637787

A;Accession: S58888

A;Accession: S58888

A;Accession: S58888

A;Accession: S58888

A;Accession: S58888

A;Accession: S58888

A;Cross-references: EMBL:X89399

F;328-539/Domain: ras-specific GAP catalytic domain homology <GAP>

F;571-670/Domain: pleckstrin repeat homology <PLK>
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Pred. No. 2.4e+02;
1; Mismatches 2;
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Best Local Similarity 62.5%;
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244 GRWPTIWG 251
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Job time: 40 secs
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3oc, H.P.; Redder,
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd
               Copyright
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using sw model - protein search, OM protein ; Search time 187 Seconds (without alignments) 24.615 Million cell update 2005, 11:52:29 e, January Run on:

updates/sec

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gywltiwg SEQ32 54 score: Sequence: Title: Perfect

Scoring table:

Gapext 0.5 BLOSUM62 Gapop 10.0 1825181 segs, 575374646 residues Searched:

1825181 of hits satisfying chosen parameters Total number

length: 0 length: 2000000000 seq sed Minimum DB Maximum DB Maximum

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

UniProt_02:*
1: uniprot_gprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description		as08923 lactoba	h2n7 oryza	r pg	398 pare	zopinm	g G	mus	Fattue	O95255 homo sapien	enterococ	_	_	_			ğ	66	E T	7 bordetell	583	10	059255 pyrococcus	N	Q88h71 pseudomonas	2a22	8013	m566	£21	9qbu	3281
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Q9ARZ0	Q6C129	Q8YX40	Q8ZUS8	Q7NSJ2	Q9KGV3	Q6TK71	AAR30325	Q6HP27	Q73E85	0811Н9	AAS39409	ARCD LACSK	Q8DW <u>P</u> 9
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ALIGNMENTS

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SEQUENCE FROM N.A.

C STRAIN-NCC 533;

PubMed=14966310;

Pridmore R.D., Berger B., Desiere F., Vilanova D., Barretto C.,

Pridmore R.D., Berger B., Desiere F., Vilanova D., Barrangou R.,

Pridet A.-C., Zwahlen M.-C., Rouvet M., Altermann E., Barrangou R.,

Mollet B., Mercenier A., Klaenhammer T., Arigoni F., Schell M.A.;

"The genome sequence of the probiotic intestinal bacterium

Lactobacillus johnsonii NCC 533.";

Lactobacillus johnsonii NCC 533.";

Proc. Natl. Acad. Sci. U.S.A. 101:2512-2517(2004).

R EMBL; AE017203; AAS08923.1; -.

R InterPro; IPR004254; HlyIII related.

InterPro; IPR005744; HyIII .

R Ffam; PF03006; HlyIII; 1.

R TIGRO1065; HlyIII; 1.

TIGRFAMS; TIGRO1065; hlyIII; 1.

W Complete proteome.

SEQUENCE 221 AA; 24721 MW; 1DBC78FF9810E152 CRC64;
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                                                                             Hemolysin-like protein.
OrderedLocusNames=LJ1101;
Lactobacillus johnsonii.
Bacteria; Firmicutes; Lactobacillales; Lactobacillus.
NCBI_TaxID=33959;
[1]
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Last sequence update)
Last annotation update)
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Pred. No. 70;
2; Mismatches
                          221 AA
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074JK6;
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05-JUL-2004
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RESULT 1
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Last sequence update) Last annotation update) Created) PRT; 27, 27, 27, PRELIMINARY; AASO8923
ID AASO8923
ID AASO8923;
AC AASO8923;
DT 02-MAR-2004 (TrEMBLrel.
DT 02-MAR-2004 (TrEMBLrel.
DT 02-MAR-2004 (TrEMBLrel.
DT 02-MAR-1014 (Tremblrel.
DE Hemolysin-like protein.
GN LJ1101. (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.

Lactobacillus johnsonii. Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae; Lactobacillus. NCBI_TaxID=33959;

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NCBI_TaxID=382;
[1]
SEQUENCE FROM N.A.
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Q92ZT6;
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                              Pridmore R.D., Berger B., Desiere F., Vilanova D., Barretto C., Pittet A.-C., Zwahlen M.-C., Rouvet M., Altermann E., Barrangou Mollet B., Mercenier A., Klaenhammer T., Arigoni F., Schell M.A. "The genome sequence of the probiotic intestinal bacterium Lactobacillus johnsonii NCC 533.";
Proc. Natl. Acad. Sci. U.S.A. 101:2512-2517(2004).
EMBL; AE017203; AAS08923.1; -. SEQUENCE 221 AA; 24721 MW; 1DBC78FF9810E152 CRC64;
                                                                                                                                                                                                                                                                 01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein OJ1138_B05.118.
Name=OJ1138_B05.118;
Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophy
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Parachlamydia sp. (strain UWE25) (subsp. Acanthamoeba sp.).
Bacteria; Chlamydiae; Chlamydiales; Parachlamydiaceae; Parachla
NCBI_TaxID=264201;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 733;
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Sasaki T., Matsumoto T., Katayose Y.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases
EMBL; AP005486; BAC16197.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E95884DAD1DC2AC9 CRC64;
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Interpro; IPR007658; DUF594
Pfam; PF04578; DUF594; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 85.7%; 6; Conservative
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05-JUL-2004 (TrEMBLrel. 2
05-JUL-2004 (TrEMBLrel. 2
Hypothetical protein.
ORFNames=pc1174;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein.
SEQUENCE 733 AA; 8
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                                                                                                                                     Similarity
5; Conserv
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                                                                                                                                                                                          GFWLLVWG
 SEQUENCE FROM N.A. STRAIN=NCC 533; PubMed=14966310;
                                                                                                                                                                      GYWLTIWG
                                                                                                                                                                                                                                                                                                                                                               _TaxID=39947;
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Q6MC01;
05-JUL-2004
05-JUL-2004
05-JUL-2004
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01-MAR-2003
01-MAR-2003
01-MAR-2004
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Best Local S
Matches 6
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                                                                                                                              Query Match
Best Local
Matches
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Q6MC01
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14-APR-2004 (TrEMBLrel. 27, Last sequence update)
14-APR-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
PC1174.
Parachlamydia sp. UWE25.
Bacteria; Chlamydiae; Chlamydiales; Parachlamydiaceae; Parachlamydia.
NCBI_TaxID=264201;
                                                                                                                                                                                                                          Gaps
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STRAIN=UWE25;
Horn M., Collingro A., Schmitz-Esser S., Beier C.L., Purkhold U.
Fartmann B., Brandt P., Nyakatura G.J., Droege M., Frishman D.,
Rattei T., Mewes H., Wagner M.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX908798; CAF23898.1; -.
Hypothetical protein.
SEQUENCE 284 AA; 33607 MW; 569E29F0D7F6AECA CRC64;
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Frishman D
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
                                                                                                                                                                          284;
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                                                                                                                                                                                                                         Indels
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STRAIN=UWE25;
Horn M., Collingro A., Schmitz-Esser S., Beier C.L., Pur Fartmann B., Brandt P., Nyakatura G.J., Droege M., Frish Rattei T., Mewes H., Wagner M.; "Genome sequence of an amoeba symbiont and its use for rithe evolutionary history of chlamydiae.";
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
"Genome sequence of an amoeba symbiont and its use for the evolutionary history of chlamydiae.";
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases
EMBL; BX908798; CAF23898.1; -.
Hypothetical protein.
SEQUENCE 284 AA; 33607 MW; 569E29F0D7F6AECA CRC64;
                                                                                                                                                                          Length
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Probable transport protein.
OrderedLocusNames=RA0363; ORFNames=SMa0684;
Rhizobium meliloti (Sinorhizobium meliloti).
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Pred. No. 1.3e+02;
2; Mismatches 0;
                                                                                                                                                                         Score 42; DB 2; Le
Pred. No. 1.3e+02;
2; Mismatches 0;
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Best Local Similarity 71.'
Matches 5; Conservative
                                                                                                                                                                                                Similarity 71. 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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273 YWLSLWG 279
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273 YWLSLWG
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Best Local
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Barloy-Hubler F., Barnett M.J., Becker A., Boistard P., Bothe G.,
Boutry M., Bowser L., Buhrmester J., Cadieu E., Capela D., Chain P.,
Cowie A., Davis R.W., Dreano S., Federspiel N.A., Fisher R.F.,
Gloux S., Godrie T., Goffeau A., Golding B., Gouzy J., Gurjal M.,
Hernandez-Lucas I., Hong A., Huizar L., Hyman R.W., Jones T., Kahn D.,
Kahn M.L., Kalman S., Keating D.H., Kiss E., Komp C., Lelaure V.,
Masuy D., Palm C., Peck M.C., Pohl T.M., Portetelle D., Purnelle B.,
Ramsperger U., Surzycki R., Thebault P., Vandenbol M.,
Vorhoelter F.J., Weidner S., Wells D.H., Wong K., Yeh K.-C., Batut J.,
"The composite genome of the legume symbiont Sinorhizobium meliloti.";
Science 293:668-672(2001).
R EMBL; AE007228; AAK65021.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M.,
Kahn D.,
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STRAIN=1021;
MEDLINE=21396509; PubMed=11481432;
Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Well:
Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R.,
Kalman S., Keating D.H., Palm C., Peck M.C.,
Kalman S., Keating D.H., Pelm M.L.,
Kalman S., Keating M.H., Pelm M.L.,
Kalman S., Keating M.H., Pelm M.L.,
Kalman S., Keating M.H., Pelm M.L.,
Kalman S., Keating M.H.,
Kalman M.H
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GO; GO:0005279; F:amino acid-polyamine transporter activity;
GO; GO:0006865; P:amino acid transport; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR002293; AA/rel_permease1.
InterPro; IPR004841; Permease_region.
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Anjard C., Loomis W.F.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases
-1- SIMILARITY: Belongs to the ABC transporter family.
EMBL; AF474339; AAL85710.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF00324; AA permease; 1.
PF00324; AA permease; 1.
ite proteome; Plasmid; Transmembrane; Transport.
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Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium
NCBI_TaxID=44689;
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on update)
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No. 1.9e+02;
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16021; C:integral to membrane; IEA.
105524; F:ATP binding; IEA.
104009; F:ATP-binding cassette (ABC)
100166; F:nucleotide binding; IEA.
106810; P:transport; IEA.
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Last annotation
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Pred.
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MEDLINE=21368234; PubMed=11474104;
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21,
26,
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les 5; Conser
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GO; GO:0016021; C
GO; GO:0004009; F
GO; GO:0000166; F
GO; GO:0000166; F
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Q8T6H2;
01-JUN-2002
01-JUN-2002
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Best Local
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Schein J.E., Jones S.J.M., Marra M.A.; and initial analysis of more than 15,000 full-length human
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SEQUENCE OF 685-1498 FROM N.A.

SEQUENCE OF 685-1498 FROM N.A.

STRAIN=FVB/N; TISSUE=Liver;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Villalon B., Young A.C., Shevchenko Y., Bouffard G.G.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
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Sciurognathi; Muridae; Murinae; Mus
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01-OCT-2004 (Rel. 45, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Multidrug resistance-associated protein 6 (ATP-binding cassette, family C, member 6).
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Morikawa A., Suzuki H., Hirohashi T., Sugiyama Y.;
"Mus musculus mRNA for multidrug resistance-associated protein
                                                                                                                                                                                                                                                                                                                                                                       Length 1308;
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5.2e+02;
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Pred. No. 5.20
0; Mismatches
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InterPro; IPR003593; AAA ATPase.
InterPro; IPR011527; ABC membrane 1.
InterPro; IPR01140; ABC TM transpt.
InterPro; IPR003439; ABC transporter.
Pfam; PF00664; ABC membrane; 2.
Pfam; PF00005; ABC tran; 2.
SMART; SM0382; AAA; 2.
PROSITE; PS50929; ABC TMIF; 2.
PROSITE; PS50929; ABC TRANSPORTER 1; 1.
PROSITE; PS50893; ABC TRANSPORTER 2; 2.
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Beck C., Le Saux O., Varadi A.,
"Abcc6.";
(er) AfCS-Nature Molecule Pages
                                                                                                                                                                                                                                                                                                                   149576 MW;
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Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
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01-OCT-2004 (Rel. 45, C
01-OCT-2004 (Rel. 45, I
01-OCT-2004 (Rel. 45, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MRP6), complete cds.
Submitted (JUN-1999)
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Proc. Natl. Acad
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764 YWLTIW
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- FUNCTION: May participate directly in the active transport of drugs into subcellular organelles or influence drug distribution indirectly (By similarity).

-!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

-!- TISSUE SPECIFICITY: High in liver and lower in duodenum and
                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: Belongs to the ABC transporter family. MRP subfamily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Hepatic expression of multidrug resistance-associated protein-like proteins maintained in eisai hyperbilirubinemic rats."; Mol. Pharmacol. 53:1068-1075(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MRP6 RAT STANDARD; PRT; 1502 AA.
088269;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2004 (Rel. 39, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Multidrug resistance-associated protein 6 (ATP-binding cassette, family C, member 6) (MRP-like protein-1) (MLP-1).
Name=Abcc6; Synonyms=Mrp6, Mlp1;
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mrp6 in
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MEDLINE=98279126; PubMed=9614210;
Hirohashi T., Suzuki H., Ito K., Ogawa K., Kume K., Shimizu T.,
                                                                                                                                                                                                                        .;
0
                                                                                                                                                                 Length 1498
I -> T (in Ref. 2).
f -> Q (in Ref. 2).
L -> V (in Ref. 2).
N -> S (in Ref. 2).
N -> S (in Ref. 2).
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STRAIN=Sprague-Dawley; TISSUE=Liver;
MEDLINE=20159081; PubMed=10692506;
Madon J., Hagenbuch B., Landmann L., Meier P.J., Stieger
"Transport function and hepatocellular localization of mr
                                                                                                                                                                                                                        Indels
                                                                                                                                                                  Score 42; DB 1; Lu
Pred. No. 5.9e+02;
; Mismatches 0;
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EMBL; U73038; AAD12747.1; -.
PIR; T42216; T42216.
HSSP; P08716; 1MT0.
RGD; 620268; Abcc6.
InterPro; IPR003593; AAA ATPase.
InterPro; IPR001140; ABC_TM_transpt.
InterPro; IPR003439; ABC_transporter.
InterPro; IPR005292; MRP_assoc.
Pfam; PF00664; ABC_membrane; 2.
Pfam; PF00005; ABC_tran; 2.
 HHJZWW.
                                                                                                                                                               Similarity 71.4%; 5; Conservative
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GYWLSLW
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095255; P78420; Q9UMZ7;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2004 (Rel. 39, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Multidrug resistance-associated protein 6 (ATP-binding cassette family C, member 6) (Anthracycline resistance-associated protein (Multi-specific organic anion tranporter-E) (MOAT-E).
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17 (By similarity)
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(Sytoplasmic (By similarity).
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Catarrhini; Hominidae;
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Cytoplasmic (Bv ~ ABC trans
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6e+02;
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Pred. No. 6e+0
2; Mismatches
Prodom; Pddddd; ABC transfer, SMART; SM00382; AAA; Z.

FROSITE; PS5029; ABC TWIF; 2.

PROSITE; PS5029; ABC TRANSPORTER_1; PROMAIN 59 78 1 (By formally a compared and a compared 
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Primates;
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata
Mammalia; Eutheria; Primates
NCBI_TaxID=9606;
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RESIDENCE FROM N.A.

MEDILINE-2010222; PubMed-2022204;

MEDILINE-2010222; PubMed-2022204;

MEDILINE-2010222; PubMed-2022204;

MEDILINE-2010222; PubMed-1043829;

MEDILINE-2012270; PubMed-1042714;

MEDILINE-201270; PubMed-1042704;

MEDILINE-201270; PubMed-10
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J. Hum. Genet. 46:699-705(2001).
J. FUNCTION: May participate directly in the active transport of indirectly. Transports glutathione conjugates as Leukotriene-c4 (LTC4) and N-ethylmaleimide S-glutathione (NEM-GS).
J. SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
J. SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
J. SISSUE SPECIFICITY: Expressed in kidney and liver. Very low capression in other tissues.
J. DISEASE: Defects in ABCC6 are a cause of autosomal dominant pseudoxanthoma elasticity of elasticitication of elastic fibers in skin, arteries and loss of elasticity, arterial insufficiency and retinal hemorrhages leading to macular degeneration.
J. DISEASE: Defects in ABCC6 are a cause of autosomal recessive pseudoxanthoma elasticum (AR-PXE) [MIM:264800].
J. SIMILARITY: Belongs to the ABC transporter family. MRP subfamily.
J. SIMILARITY: Belongs to the ABC transporter family. MRP subfamily.
J. CAUTION: Ref. 2 sequence differs from that shown due to erroneous gene model prediction.
J. DATABASE: NAME=Mutations of the ABCC6 gene;
NOTE=Retina International's Scientific Newsletter;
WWW="http://www.retina-international.com/sci-news/abcc6mut.htm".
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                                                                                                                                                                                                                                                     1114;
3-1302;
N-1361
VAL-319;
                                                                                                                                                                                                                                            VARIANTS PXE LYS-411; GLN-518; SER-568; PRO-673; GLN-765; PRO-1114; TRP-1121; PRO-1138; GLN-1138; ASP-1203; PHE-1298; ILE-1301; ARG-136; PRO-1303; GLN-1314; TRP-1314; SER-1321; CYS-1339; HIS-1347; ASN-136; AND THR-1424, AND VARIANTS ASP-61; ARG-207; GLY-265; GLU-281; VAL-32; LYS-497; ALA-614; GLN-632; HIS-953; CYS-1241 AND GLN-1268.

MEDLINE=21426347; PubMed=11536079; CYS-1241 AND GLN-1268.

A Goering H.H.H., Johnson E.W., De Paepe A., Pope F.M., A Spectrum of ABCC6 mutations is responsible for pseudoxanthoma elasticum."; Am. J. Hum. Genet. 69:749-764(2001).
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VARIANTS PXE 60-ARG--TYR-62 DEL; ARG-364 AND ARG-1354, AND VARI
                                                                             MEDLINE=20283940; PubMed=10811882; DOI=10.1073/pnas.100041297; Ringpfeil F., Lebwohl M.G., Christiano A.M., Uitto J.; "Pseudoxanthoma elasticum: mutations in the MRP6 gene encoding transmembrane ATP-binding cassette (ABC) transporter."; Proc. Natl. Acad. Sci. U.S.A. 97:6001-6006(2000).
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with variation
                                                          GLN-1268.
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MEDLINE=21632106; PubMed=11776382;
Wang J., Near S., Young K., Connelly P.!
"ABCC6 gene polymorphism associated witllipoproteins.";
J. Hum. Genet. 46:699-705(2001).
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U91318; AAC15785.1; AI
AF168791; AAD51293.1;
P08716; 1MT0.
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HSSP; P08716; 1MTO. Genew; HGNC:57; ABCC6 MIM; 603234; -.

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STRAIN=V583 / ATCC 700802;
MEDLINE=22550857; PubMed=12663927; DOI=10.1126/science.1080613;
MEDLINE=22550857; PubMed=12663927; DOI=10.1126/science.1080613;
Paulsen I.T., Banerjei L., Myers G.S.A., Nelson K.E., Seshadri R., Read T.D., Fouts D.E., Bisen J.A., Gill S.R., Heidelberg J.F., Tettelin H., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J., Tettelin H., Dodson R.J., Tran B., Upton J., Hansen T., Shetty J., Nelson W.C., Vamathevan J.J., Tran B., Upton J., Hansen T., Shetty J., Khouri H.M., Utterback T.R., Radune D., Ketchum K.A., Dougherty B.A.,
Gaps
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OrderedLocusNames=EF3185;
Enterococcus faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus
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Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe
Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.
Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
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Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
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Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach
Mincker P., Souciet J.L.;
"Genome evolution in yeasts.";
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01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Similar to sp|P38071 Saccharomyces cerevisiae YBR026c.
ORFNames=YALIOC19624g;
Yarrowia lipolytica (Candida lipolytica).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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Fraser C.M.;
"Role of mobile DNA in the ev
Enterococcus faecalis.";
Science 299:2071-2074(2003).
EMBL; AE016957; AAO82859.1; -
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STRAIN=DSM 1728;
MEDLINE=20479972; PubMed=11029001;
Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C., Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;
"The genome sequence of the thermoacidophilic scavenger Thermoplasma acidophilum.";
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SEQUENCE FROM N.A.

STRAIN=ATCC 35092 / DSM 1617 / P2;

MEDLINE=2133296; PubMed=11427726;

She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,

A Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,

De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,

Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

A Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

A Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,

A Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,

A Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.,

"The complete genome of the crenarchaeon Sulfolobus solfataricus P2

Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
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Thermoplasmataceae; Thermoplasma.
NCBI_TaxID=2303;
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Sulfolobus solfataricus.
Archaea; Crenarchaeota; Thermoprotei; Sulfolobales;
                                                   annotation update)
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Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation updat Transport protein related protein. OrderedLocusNames=Ta0692; Thermoplasma acidophilum.
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PIR; E90446; E90446.

GO; GO:0016021; C:integral to membrane; IE
GO; GO:0006215; F:transporter activity; IE
GO; GO:0006810; P:transport; IEA.
InterPro; IPR007114; MFS.
InterPro; IPR005828; Sub_transporter.

Pf: Description of the context o
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EMBL; AL445065; CAC11830.1; -.
GO; GO:0016021; C:integral to membrane;
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GO; GO:0006810; P:transport; IEA.
InterPro; IPR007114; MFS.
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MEDLINE=22225144; PubMed=12240834;

Matanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y.,

Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N.,

Kiyokawa C., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;

"Complete genome structure of the thermophilic cyanobacterium

Thermosynechococcus elongatus BP-1.";

DNA Res. 9:123-130(2002).

EMBL; AP005369; BAC07560.1; -.

EMBL; AP005369; BAC07560.1; -.

R InterPro; IPR001173; Glyco_trans 2.

Pfam; PF00535; Glycos_transf_2; 1.

Complete proteome.

SEQUENCE 736 AA; 85049 MW; D31C506166FD9624 CRC64;
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Q8DMV4;
Q8DMV4;
Q1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Cellulose synthase.
OrderedLocusNames=tll0007;
Synechococcus elongatus (Thermosynechococcus elongatus).
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
NCBI_TaxID=32046;
[1]
SEQUENCE FROM N.A.
  Length 419;
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Score 41; DB 2; Le
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Scoring table:

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2002273 segs, 358729299 residues Searched:

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ALIGNMENTS

Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3; angiogenesis; lymphangiogenesis; vascular endothelial growth factor; cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic; vulnerary; cell surface receptor; cancer; neovascularisation; liver disease; hypertension; post-trauma; chronic hepatitis; haemangion diabetes; PDGF; platelet derived growth factor. VEGFR-3 binding peptide SEQ ID NO:67. Z 7 standard; peptide; entry) (first 09-JAN-2003 ABP53964; ABP53964 RESULT 1 CCCXSXTTTTXBXBXBXBXTTTTXSSXXXXXXXBXBXCCCX

Homo sapiens Synthetic.

haemangioma;

is any amino acid" Location/Qualifiers
4. .6
/note= "X is anv am" Key Misc-difference

WO200257299-A2

25-JUL-2002

2002WO-IB000099 16-JAN-2002;

17-JAN-2001; 2001US-0262476P

(LUDW-) LUDWIG INST CANCER RES (LICN) LICENTIA LTD. (FICN)

Ħ; Kubo ы Koivunen 저, Alitalo

WPI; 2002-691521/74

New isolated peptide that inhibits VEGF-C and VEGF-D, useful for diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity, such as cancer and diseases of neovascularization.

Claim 21; Page 81; 149pp; English.

and (T) The present invention describes an isolated peptide (I) that binds inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). have cytostatic, hepatotropic, antiinflammatory, hypotensive,

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                                                                    pancreas, colon, stomach, breast, endometrium, prostate, testicle, skin, head and neck, oesophagus, bone, marrow or blood, and disease neovascularisation, e.g. liver diseases, hypertension, post-trauma, chronic hepatitis, haemangiomas and diabetes. The present sequence represents a specifically claimed VEGFR-3 binding peptide from the
                                             lung,
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antidiabetic and vulnerary activities, and can be used in gene Compositions and methods from the present invention are useful diagnosing, evaluating and treating disorders mediated by the a the cell surface receptor VEGFR-3 such as cancer, e.g. brain, liver, spleen, kidney, lymph node, small intestine, blood cells pancreas, colon, stomach, breast, endometrium, prostate, testic skin, head and neck, oesophagus, bone, marrow or blood, and dis
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the treatment
antidiabetic and vulnerary activities, and can be used in gene therapy. Compositions and methods from the present invention are useful for diagnosing, evaluating and treating disorders mediated by the activity of the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung, liver, spleen, kidney, lymph node, small intestine, blood cells, pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary, skin, head and neck, oesophagus, bone, marrow or blood, and diseases of neovascularisation, e.g. liver diseases, hypertension, post-trauma, chronic hepatitis, haemangiomas and diabetes. The present sequence represents a specifically claimed VEGFR-3 binding peptide from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Somatostatin analogue; therapy; cyclic peptide; autoimmune disease; endocrine disorder; cancer; diabetic-associated complication; diagnosis; gastrointestinal disorder; inflammatory disease; pancreatitis; atherosclerosis; restenosis; post-surgical pain; VIP secretion inhibitor; hormone-secreting tumour; hormone-dependent tumour; diarrhoea; vasoactive intestinal peptide; non-insulin dependent diabetes mellitus.
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98US-00203389
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57.1%;
                                                                                                                                                                                                                                                                                                                                                              standard; peptide;
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erior pituitary
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                                                                                                                                            present invention
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                                                                                                                                                                                                                                                             GYWLTIW
                                                                                                                                                                                                                                                                                        GYWXXXW
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                                                                                                                                                                          8 AA;
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02-DEC-1998
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Best Local
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or disulphide. At least one building unit is connected via a bridging group to form a cyclic structure with a moiety selected from a second building unit, side chain of or N-terminal amino acid residue. A composition containing the analogue may be used for preventing disorders such as cancers, autoimmune diseases, endocrine disorders, diabeticased complications, gastrointestinal disorders, inflammatory diseases, pancreatitis, atherosclerosis, restenosis and post-surgical associated complications, gastrointestinal disorders, inflammatory diseases, pancreatitis, atherosclerosis, restenosis and post-surgical analogue is used for the dispussing cancer. The backbone cyclic analogues can be used for the treatment patients with hormone-secreting and hormone-dependent tumours. They reduce diarrhoea through the inhibition of vasoactive intestinal peptide (VIP) secretion and by direct inhibition of vasoactive intestinal peptide (VIP) secretion and by direct cand 5 receptors may be used for treatment of non-insulin dependent diabetes mellitus. They are useful for the prevention of atherosclerosis and restenosis. The analogues are metabolically stable, selective in their in-vivo activities and safe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               restenosis;
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r subtype;
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[fluorenylmethoxycarbonyl)"
                                                                                                                                                                                                                                                                                                           Length
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                                                                                                                                                                                                                                                                                                          Score 32; DB 3;
Pred. No. 1.7e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       somatostatin analogue PTR
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98US-00203389.
99WO-IL000329.
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illarity 57.1%;
Conservative
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GELLERMAN
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02-DEC-1998;
15-JUN-1999;
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(AFAR/)
(GELL/)
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ABP53418
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Gellerman G;

Afargan MM,

Hornik

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The present invention describes backbone cyclised somatostatin analogues

(I) that incorporates at least one building unit containing one nitrogen
atom of the peptide backbone connected to a bridging group (comprising an
amide, thioether, thioester or disulfide) where at least one building
cunit is connected via the bridging group to form a cyclic structure with
a moiety selected from the group consisting of a second building unit,
the side chain of an amino acid residue of the sequence or the N-terminal
cunit and acid residue. (I) has antiarteriosclerotic, immunosuppressive,
cytostatic, antidiabetic, antidialmamatory and analogue cativities, and
can be used as a somatostatin receptor ligand. (I) are useful in the
treatment of atherosclerosis, autoimmune diseases, cancers, diabetic-
associated complications, endocrine disorders, inflammation,
cassociated complications, endocrine disorders, inflammation,
cassociated complications, endocrine disorders, inflammation,
crestenosis. (I) can also be used in the diagnosis of cancer, by imaging
the existence of metastases, it being labeled with a detectable probe.
The present sequence represents a backbone cyclised somatostatin analogue
from the present invention
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neuraminidase (HN) protein of the paramyxoviridae. The specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GapB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antigenic site; haemagglutinin-neuraminidase; HN; paramyxoviridae; virus epitope; attachment protein; vaccine; immunodominant epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     one virus
                                              cyclized somatostatin analogs are e.g. useful in atherosclerosis, autoimmune diseases and cancers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 5; Le.
1.7e+06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            site of HN protein loop beta-4L23
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                                                                                               30pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | proteinaceous substance - from an attachment protein
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ilarity 57.1%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW97529 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                               Page 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-120896/10.
                2002-681319/73
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Best Local Similarity
Matches 4; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                        7 A.
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                                               New backbone
treatment of
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                                                                                               Example 12;
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derived f
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Mismatches

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Conservative
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Misc-difference
                     3 WLTIW
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                                      WLDIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5 AA;
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                                                                                                                                                                                                                                                                            17-DEC-1993;
                                                                                                                                                                                                                                                                                               21-DEC-1992;
                                                                                                                                                                                                                                        WO9414843-A1
                                                                                                                                                                 Endothelin;
                                                                                                                      25-MAR-2003
06-MAR-1995
                                                                                                                                                                                                                                                            07-JUL-1994
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   4;
                                                                                                                                                                                    Synthetic.
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Best Local S
Matches 4
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    comprising at
                    The
                             viruses,
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-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and
describes 3-D models identifying a proteinaceous substance comprisileast one virus epitope derived from the attachment protein, which corresponds to an antigenic site present on one of the loops of HN. antigenic sites can be used to produce vaccines, to detect the viruand to select the immunodominant epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The peptide is an endothelin antagonist useful in controlling hypertension, myocardial infarction, congestive heart failure, shock, subarachnoid haemorrhage, asthma, arrhythmias, acute ren failure, preeclampsia, diabetes and metabolic, endocrinological neurological disorders. Administration is oral parenteral or by inhalation in doses of 0.01-20 (esp. 0.01-10) mg/kg/ day. It ma prepared by conventional peptide synthesis. (Updated on 25-MAR-correct PN field.)
                                                                                                                                                                                                                                                          Hypertension; myocardial infarction; congestive heart failure; endotoxic shock; subarachnoid haemorrhage; asthma; arrhythmias; acute renal failure; preeclampsia; diabetes; metabolic; endocrineurological; disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or treating
heart failure
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                                                                                            Indels
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                                                                          Score 31; DB 2; L
Pred. No. 1.7e+06;
); Mismatches 0;
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Pred. No. 1.7e+06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Taylor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      etc
                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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nsion, metabolic and endocr
neurological disorders, et
                                                                                                                                                                                                                                                                                                                                           "Ac-D-Trp"
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                                                                           57.4%;
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80.0%;
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(first entry)
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                                                                                            Conservative
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Best Local Similarity
5; Conserva
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18-DEC-1991;
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13-APR-1993
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Best Local
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                                                                                                                                                                                                                                                                                                                                                  useful as antagonist.
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Pred. No. 1.7e+06;
); Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                            antagonist
                                                                                                                                                                                                                                                                                                                                                  Endothelin C-terminal peptide analog,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         le derivs. inhibiting hypertension, asthma,
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ilarity 80.0%;
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                                                                                                                                                                                              AAR69224 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                             ET-1; receptor;
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                                                                                                                                                                                                                                                                                                                                     reagent
o detect HIV
                                                                                                                                                                                                                                                                                AAW56525-36 represent antigenic Human immunodeficiency virus type 1 (HIV-1) peptides used in the test device of the invention. This test device comprises, in a housing, an absorbent pad, a reagent layer containing immobilised test antigens and a filter. The housing has an opening, adjacent to the filter, for applying an aqueous sample, and the filter is held in contact with the reagent layer by a sleeve. The filter protrudes from the sleeve such that it exerts a greater pressure on the reagent layer than does the sleeve. The device is specifically used to detect HIV infection from presence of specific antibodies in whole blood, but many other analytes can also be detected, e.g. amino acids, nucleic acid, hormones, vitamins, microbial pathogens and drugs (therapeutic or
                                                                                                                                                                                                                                 and increased
to human
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                                 Antigenic HIV-1 peptide used in diagnostic test device of invention.
                                                  antibody;
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antibodies
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                                                 detection; HIV infection; 1; microbial pathogen; dru
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Pred. No. 1.7e+06;
; Mismatches 0;
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                                                                                                                                                                                                                           chemical resistance, especially for detecting immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tyrosine tRNA synthetase binding peptide
                                                                                                                                                                               (UVHE-) UNIVERSAL HEALTHWATCH INC.
                                                                                                                                                                                                                                                                 50pp; English.
                                                          vitamin;
                                                                                    7
                                                                                   Human immunodeficiency virus
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97US-00912580
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illarity 80.0%;
Conservative
                                                  device;
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Jest Local Similarity
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                                                 HIV-1; antigen; whole blood; ho
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18-AUG-1997
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                                                                           Synthetic
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immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
.c T lymphocyte; CTL; immune response; epitope; antigen;
tion; immunisation; virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a method of identifying a ligand that can mediate the biological activity of target protein via inhibition of the binding of target protein to a binding partner ligand comprising screening first combinatorial library having first member ligands for binding to target protein to identify target-binding ligand(s). The method is useful for identifying ligands that can mediate the biological activity of target proteins via inhibition of the binding of target protein to a binding partner ligand. The invention does not require that the natural binding partner be used as reagent. The need for the natural binding partner is obviated with the use of complementary combinatorial libraries. The present sequence is used in the exemplification of the
                                                                                                                                                                                                                                                                                       Identification of ligand that can mediate biological activity of target protein, comprises screening first combinatorial library having first member ligands for binding to target protein to identify target-binding
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1.7e+06;
3;
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                                                                                                                                                                                                                                                                                                                                                                                                94; 98pp; English
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vaccine; HIV infection; immunisation;
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97WO-US019638.
98US-00050359.
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ilarity 57.1%;
Conservative
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(first entry)
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                                                                                                                                                                                                         Kay BK,
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31-OCT-1997;
31-MAR-1998;
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15-JUL-2002
09-SEP-2003
                                                                                                                                                                                                           Fowlkes DM,
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ABP22594
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accines. An
ability to
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                                                                                                  The present invention describes a composition (I) comprising an amino acid human immunodeficiency virus-1 (HIV-1) group comprising an amino acid sequence selected from 51 defined amino acid sequences (ABL25347 to ABP25397). (I) has virucide activity and can be used in vaccines. (I) may be used for immunising subjects against HIV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens is directed largely toward variable regions of the antigen, antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in a group-based vaccine any be selected from conserved regions of viral or tumour-associated antigens, which therefore reduces the likelihood of escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABP11501 to ABP25412 invention. (Updated on 11-SEP-2003 to standardise OS field)
                                                                                                                                     (I) may
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vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; a
vaccine; HIV infection; immunisation; virucide.
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Chesnut
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                                                   cions comprising human immunodeficiency useful for vaccinating against HIV-1.
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 Livingston BD,
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S, Livir
Grey HM;
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                                                                                  448pp; English
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 Southwood
Kubo RT,
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larity 80.0%;
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                                                               peptide groups,
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                                                                                   Claim 32; Page
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                                                    Vaccine
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The present invention describes a composition (I) comprising an amino acid sequence selected from 51 defined amino acid sequences (ABL25347 to ABP25397). (I) has virucide activity and can be used in vaccines. (I) may be used for immunising subjects against HIV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in an group-based vaccine may be selected from conserved regions of viral or tumour-associated antigens, which therefore reduces the likelihood of escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (CTL and HTL), and further, to modify the composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABP11501 to ABP25412 represent peptide sequences used in the exemplification of the present invention. (Updated on 11-SEP-2003 to standardise OS field)
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                                            (HIV-1)
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0
                                             virus-1
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                                         immunodeficiency
r against HIV-1.
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Pred. No. 1.7e+06;
; Mismatches 0;
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Kubo RT, Grey HM;
                                          compositions comprising human igroups, useful for vaccinating
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                                                                                                                    English.
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                                                                                                                     32; Page 161;
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2001-354887/37
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15-JUL-2002
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WPI;
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against HIV-1

vaccinating

useful for

groups,

peptide

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membrane immunodeficiency virus-1 (HIV-1) group comprising an amino acid sequence selected from 51 defined amino acid sequences (ABI25347 to ABP25397). (I) has virucide activity and can be used in vaccines. (I) may be used for immunising subjects against HIV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines compositions. There is evidence that the immune response to whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, antigens is directed largely toward variable regions of the antigen, antigens is directed largely toward variable regions of the antigen, antigens is directed largely toward variable regions of the antigen, antigens are selected from conserved regions of viral or tumour-associated antigens, which therefore reduces the likelihood of the group-based vaccine approach is the ability to additional advantage of an group-based vaccine approach is the ability to combine selected groups (CTL and HTL), and further, to modify the composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABPI1501 to ABP25412 represent peptide sequences used in the exemplification of the present invention. (Updated on 11-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antigen;
                                                                                                     (I) comprising a prepared
comprising an amino acid
sequences (ABL25347 to
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vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
vaccine; HIV infection; immunisation; virucide.
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                  immunodeficiency virus-1
g against HIV-1.
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Pred. No. 1.7e+06;
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Grey HM;
              comprising human i
11 for vaccinating
                                                                                                     3 a compo
(HIV-1)
                                                                  32; Page 252; 448pp; English
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Kubo RT,
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(first en
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groups, usefi
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Celis E,
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Best Local S
Matches 4
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Baker
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(HIV-1)

Vaccine compositions comprising human immunodeficiency virus-1

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The present invention describes a composition (1) comprising a prepared human immunodeficiency virus-1 (HIV-1) group comprising an amino acid sequence selected from 51 defined amino acid sequences (ABL25347 to ABP25397). (1) has virucide activity and can be used in vaccines. (1) may be used for immunising subjects against HIV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines. Compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, an group-based vaccine may be selected from conserved regions of viral or an group-based vaccine may be selected from conserved regions of viral or tumour-associated antigens, which therefore reduces the likelihood of escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (CTL and HTL), and further, to modify the composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABPI1501 to ABP25412.

Tepresent peptide sequences used in the exemplification of the present invention. (Updated on 11-SBP-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  compositions comprising human immunodeficiency virus-1 groups, useful for vaccinating against HIV-1.
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Pred. No. 1.7e+06;
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Grey HM;
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vaccine; HIV infection; immunisation;
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Kubo RT,
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                                 285; 448pp;
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Celis E,
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nes 4; Conser
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                                Page
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15-JUL-2002
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                                 Claim 32;
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DM,
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                                      The present invention describes a composition (I) comprising an prepared human immunodeficiency virus-1 (HIV-1) group comprising an amino acid sequence selected from 51 defined amino acid sequences (ABL25347 to ABP25397). (I) has virucide activity and can be used in vaccines. (I) may be used for immunising subjects against HIV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in an group-based vaccine may be selected from conserved regions of viral or tumour-associated antigens, which therefore reduces the likelihood of escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (CTL and HTL), and further, to modify the composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABP11501 to ABP25412 represent peptide sequences used in the exemplification of the present invention. (Updated on 11-SEP-2003 to standardise OS field)
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Pred. No. 1.7e+06;
1; Mismatches 0;
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Grey HM;
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vaccine; HIV infection; immunisation;
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the present invention describes a composition (1) comprising an amino acid chuman immunodeficiency virus-1 (HIV-1) group comprising an amino acid chuman immunodeficiency virus-1 (HIV-1) group comprising an amino acid chuman immunodeficiency virus-1 (HIV-1) group comprising an amino acid chuman immunodeficiency virus-1 (HIV-1) group compositions. The use of group-based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in an group-based vaccine may be selected from conserved regions of viral or tumour-associated antigens, which therefore reduces the likelihood of can group-based vaccine approach is the ability to additional advantage of an group-based vaccine approach is the ability to additional advantage of an group-based vaccine approach is the ability to combine selected groups (CTL and HTL), and further, to modify the composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABP11501 to ABP25412 represent peptide sequences used in the exemplification of the present invention. (Updated on 11-SEP-2003 to standardise OS field)
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 composition
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illarity 80.0%;
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Search completed: January 3, 2005, 12:27:56 Job time : 150 secs

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66318000 residues 478139 seqs, Searched

73656 of hits satisfying chosen parameters number Total

Minimum DB seq length: 0 Maximum@DB_seq_length: 8

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Patents Issued

/cgn2_6/ptodata/1/iaa/5A_COMB.pep:*/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:/cgn2_6/ptodata/1/iaa/backfiles1.pep: 4 0 M 4 W 9

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SUMMARIES

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Description	quence 94, App	nce 1649, A	12, App	ence 12, App	17, App	1495, A	1495, A	1650, A	27, App	3, Appl	4, Appl	5, Appl	6, Appl	1500, A	5, Appl	6, Appl	1500, A	9, Appl	1655, A	5, Appl	21, App	21, App	1, Appl	56, App	1, Appl	ppl	19, App
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ID	S-09-069-827A-9	-315-	S-08-19	29	6-670A-1	-09-082-279B-14	-09-834-	-09-350-641C-16	-08-353-40	US-08-415-099A-3	-08-41	US-08-467-472C-5	US-08-467-472C-6	US-09-082-279B-1500	US-09-384-061-5	US-09-384-061-6	0-	US-08-632-444B-9	-09-350-64	US-09-852-870A-5	US-08-191-571-21	PCT-US95-00296-21	US-09-155-106-1	-08-660-747-	US-09-125-641-1	US-09-125-641-2	US-08-481-968A-19
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SEQ ID NO: 94:

STRANDEDNESS: single

amino acid

TOPOLOGY: linear MOLECULE TYPE: peptide SEQUENCE DESCRIPTION:

Seguence 19, Appl	Sequence 19, Appl	Sequence 38, Appl	. 5185	, App	App	3, Ap	Sequence 653, App	79, A	Ap	App	653, Ap	3, Ap	Sequence 653, App	79, A	Ω	Seguence 653, App	Sequence 47, Appl
US-08-154-712B-19	US-09-947-925A-19	US-08-753-750B-38	5185431-15	US-07-718-577-6	US-08-660-747-60	US-09-082-279B-653	US-09-315-304B-653	US-09-315-304B-1579	US-09-388-788-2	US-09-350-325-39	US-09-834-784-653	US-09-515-965A-653	US-09-350-641C-653	US-09-350-641C-1579	US-09-563-222C-53	US-09-350-841A-653	US-08-073-028-47
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ALIGNMENTS

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APPLICANT: FOWLKES, Dana M
KAY, Brian K
FRELINGER, Jeffrey A
HYDE-DERUYSCHER, Robin P
HYDE-DERUYSCHER, Robin P
TITLE OF INVENTION: IDENTIFICATION OF DRUGS USING
COMPLEMENTARY COMBINATORIAL LIBRARIES
                                                                                                                                                                                                                                             CORRESPONDENCES: 178
CORRESPONDENCES: 178
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 624 Ninth Street N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20001
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/069,827A
FILING DATE: 30-Apr-1998
CLASSIFICATION NUMBER: US 09/050,359
FILING DATE: 31-MAR-1998
APPLICATION NUMBER: PCT/US97/19638
FILING DATE: 31-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: FOWLKES=4C
              US-09-069-827A-94
; Sequence 94, Application US/09069827A
; Patent No. 6617114
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acid
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2 ID NO:
                                                                                                                                                                                                                                      SEQUENCES:
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                                                                                                                                                          TYPE: amino ;
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; MOLECULE TYPE:
US-08-191-571-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
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                                                                                                                                                                                            Sequence 1649, Application US/09315304B
; Sequence 1649, Application US/09315304B
; Patent No. 6348568
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-052
; CURRENT APPLICATION NUMBER: US/09/315,304B
; CURRENT FILING DATE: 1999-05-20
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1667
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1649
; LENGTH: 8
                                                                 Gaps
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; Patent No. 5521156
; GENERAL INFORMATION:
; APPLICANT: Owen, Thomas J.
; APPLICANT: Kudlacz, Elizabeth M
; APPLICANT: Buck, Stephen H
; APPLICANT: Harbeson, Scott L
; TITLE OF INVENTION: Cyclic Neurokinin A Antagonists
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marion Merrell Dow Inc.
; STREET: P. O. Box 156300 2110 E. Galbraith Rd.
; CITY: Cincinnati
                                Length
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/191,571
FILING DATE: 03-FEB-1994
CLASSIFICATION: 514
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Pred. No. 3.8e+05;
; Mismatches 1
                                              ed. No. 3.8e+05; Mismatches 3
                               DB 4;
                             Score 29;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: United States
ZIP: 45215-6300
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                             53.7%;
illarity 57.1%;
Conservative
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Best Local Similarity 50.0%;
Matches 3; Conservative
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ATTORNEY/AGENT INFORMATION:
                Query Match
Best Local Similarity
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US-09-315-304B-1649
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US-09-315-304B-1649
US-09-069-827A-94
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US-08-191-571-12
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ORGANISM:
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STATE:
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ADDRESSEE: Marion Merrell CONTEST: 2110 East Galbraith Road, P.O. DOCTOTY: Cincinnati
STRET: 2110 East Galbraith Road, P.O. DOCTOTY: Cincinnati
STATE: OH
COUNTRY: USA
ZIP: 45215-6300
COMPUTER: BM PC COMPATIBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC COMPATIBLE
COMPUTER: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
FILING DATE:
CLASSIFICATION:
NAME: BOUGLEAUX, William R
REGISTRATION NUMBER: 35,796
RELEPHONE: 513-948-7961 or 4681
TELEPHONE: 513-948-7961 or 4681
TELEFAX: 214320
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
A mino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEE: Marion Merrell Dow Inc.
: 2110 East Galbraith Road, P.O. Box 156300
Cincinnati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Merrell Dow Pharmaceuticals Inc.
TITLE OF INVENTION: Cyclic Neurokinin A Antagonists
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                  Score 27.5; DB 1;
Pred. No. 3.8e+05;
); Mismatches 1.
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Pred. No. 3.8e+05;
0; Mismatches 1
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PCT-US95-00296-12
; Sequence 12, Application PC/TUS9500296
; GENERAL INFORMATION:
                                               M01718
NAME: Boudreaux, William R
REGISTRATION NUMBER: 35,796
REFERENCE/DOCKET NUMBER: M017:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 513-948-6566
TELEFAX: 513-948-7961 or 4681
TELEX: 214320
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
                                                                                                        or 4681
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nilarity 71.4%;
Conservative
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LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: circular
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E: peptide
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APPLICANT: Merutka, G. APPLICANT: Anwer, M. APPLICANT: Lambert, D. TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
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             APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Merutka, Gene
APPLICANT: Anwer, Mohmed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/082,2798
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1495
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Pred. No. 3.8e+05;
; Mismatches 1
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CURRENT APPLICATION NUMBER: US/09/834,784
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSEQ for Windows Version 3.0
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Pred. No. :
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Patent No. 6656906
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1495, Application US/09834784 Patent No. 6562787
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llarity 50.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
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Anwer, M.
Lambert, D.
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Merutka, G.
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  GENERAL INFORMATION:
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US-09-350-641C-1650
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LENGTH: 8
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Best Local S
Matches 3
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Best Local
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the Trp is in
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/note= "Phe is in the D conformation and
linked to DTPA;
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                                                           APPLICANT: McBride, William
APPLICANT: Dean, Richard T.
TITLE OF INVENTION: Somatostatin Derivatives
TITLE OF INVENTION: And their Radiolabeled Products
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= Variant residues
/note= "The carboxyl group of
Thr is reduced to an alcohol;
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/note= "The Phe is in the D
is L-4-chlorophenylalanine;
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3.8e+05;
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Pred. No. 3.8e
0; Mismatches
                                                                                                                                                             ADDRESSEE: Banner & Witcoff, Ltd.
STREET: 10 South Wacker Drive, Suite
CITY: Chicago
                                                                                                                                                                                                        STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/586,670A
FILING DATE: 22-APR-1996
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: No. 6241965nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 92,385-DD
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acide
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US-09-082-279B-1495
; Sequence 1495, Application US/09082279B
; Patent No. 6258782
             Sequence 17, Application US/08586670A Patent No. 6241965 GENERAL INFORMATION:
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80.0%;
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Modified LOCATION: 1..2 OTHER INFORMATION: OTHER INFORMATION: FEATURE:
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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TOPOLOGY: li
MOLECULE TYPE:
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                                                                                                                                                            ADDRESSEE:
US-08-586-670A-17
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Best Local S
Matches 4
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Gapв

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RESULT 11
US-08-415-099A-4

i Sequence 4, Application US/08415099A

j Sequence 4, Application US/08415099A

j Patent No. 5789384

j GENERAL INFORMATION:

i APPLICANT: Khavinson, V.Kh., Sery, S.V. and Morozov, V.G.

i TITLE OF INVENTION: "Pharmaceutical Dipeptide Compositions and Methods of Use Ther

i NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSE: Cytoven

STREET: .10230 N.E. Points Drive, Suite 530

CITY: Kirkland

STATE: Washington

COUNTRY: USA
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                                                                                                                                                        1.44Mb storage
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                                                      530
                                                      Suite
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MEDIUM TYPE: Diskette-3.25 inch, 1.4*
COMPUTER: IBM PC/486 Compatible
OPERATING SYSTEM: MS-DOS 5.01
SOFTWARE: Word for Windows 6.0-t
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/415,099A
FILING DATE: 31-MAR-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/415,099A
FILING DATE: 31-MAR-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/271,386
FILING DATE: 06-JUL-1994
APPLICATION NUMBER: 08/026,341
FILING DATE: March 4, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Sundsmo, John, S.
REFERENCE/DOCKET NUMBER: 15548-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 1-206-889-5804(direct)
TELEFAX: 1-206-822-3644
STATE: Washington COUNTRY: USA
                                                                                                                    ZIP: 98033
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette-3.25 inch, 1
COMPUTER: IBM PC/486 Compatible
OPERATING SYSTEM: MS-DOS 5.01
SOFTWARE: Word for Windows 6.0-t
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48.1%;
illarity 60.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
LENGTH: 6 amino acids
    NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 3; Conserv
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Patent No. 5789384
GENERAL INFORMATION:
APPLICANT: Khavinson, V.Kh., Sery, S.V. and Morozov, V.G.
TITLE OF INVENTION: "Pharmaceutical Dipeptide Compositions
                                                                                                                                                                                                                                                                             8
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Pred. No. 3.8e+05;
L; Mismatches 0;
                                                                                                                                                                                                                                                                           ore 27; DB 4; Losd. No. 3.8e+05; Mismatches 1;
TITLE OF INVENTION: PROPERTIES
FILE REFERENCE: 7872-067
CURRENT APPLICATION NUMBER: US/09/350,641C
CURRENT FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/315,304
PRIOR FILING DATE: 1999-05-20
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1757
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1650
LENGTH: 8
                                                                                                                                                                                                                                                                           Score 27;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,400
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US/08/353,400
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FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 27, Application US/08353400
Patent No. 5665357
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                             5
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ilarity 75.0%;
Conservative
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03-JUN-1994
EQ ID NO: 27
                                                                                                                                                                                                                                                                            50.0%;
larity 50.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: PROTEIN NUMBER OF SEQUENCES: 37 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
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; MOLECULE TYPE: protein
US-08-353-400-27
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
FILING DATE: 03-JUNINFORMATION FOR SEQ ID
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Best Local Similarity
3; Conserv
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                                                                                                                                                                                                                          ; ORGANISM: HIV-1
US-09-350-641C-1650
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1 GYWI
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08-353-400-27
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Best Local S
Matches
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PEPTIDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PUBLICATION INFORMATION:
AUTHORS: BEAN, MARK F.
TITLE: IDENTIFICATION OF A THIOETHER
TITLE: BY-PRODUCT
TITLE: BY
TITLE: BY
TITLE: BY
TITLE: BY
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: PEPTIDE
JOURNAL: SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
                       HYPOTHETICAL: N/A
ANTI-SENSE: N/A
FRAGMENT TYPE: INTERNAL
ORIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE
ORIGINAL SOURCE: INC.,
IMMEDIATE SOURCE: SYNTHESIZED PEPTIDE
POSITION IN GENOME: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ore 26; DB 3; L'ed. No. 3.8e+05; Mismatches 2;
                                                                                                                                                                                      LOCATION: -4

IDENTIFICATION METHOD: amino acid analysis
IDENTIFICATION METHOD: and
IDENTIFICATION METHOD: mass spectrometry
OTHER INFORMATION: water is removed and
OTHER INFORMATION: thereby
OTHER INFORMATION: a -S- bridge is present b
PUBLICATION INFORMATION:
AUTHORS: JUNG, GUNTHER
TITLE: PEPTIDES WITH SULFIDE BRIDGES AND
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYS-SER
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STRUCTURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAGES: 865 - 869
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 5: CYS-SER
PUBLICATION INFORMATION:
AUTHORS: SHIBA, TETSUO
TITLE: CHEMISTRY OF LANTHIONINE PEPTIDES
JOURNAL: BIOPOLYMERS
VOLUME: JOHN WILEY AND SONS, INC.
ISSUE: SUPPLEMENTARY
PAGES: 511 - 519
DATE: 1986
DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYS-SER
                                                                                                                                                                                                                                                                                                            is present
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Pred. No. 3
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PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
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IN SEQ ID NO:
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ilarity 50.0%;
Conservative
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FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES 1
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1990
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Best Local Similarity
Matches 3; Conser
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                                                                                                                                                      FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISSUE:
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; Patent No. 6028168
; GENERAL INFORMATION:
; APPLICANT: GOODMAN, MURRAY
; TITLE OF INVENTION: LANTHIONINE BRIDGED PEPTIDES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROOKS HAIDT HAFFNER & DELAHUNTY
STREET: 99 PARK AVENUE
; CITY: NEW YORK
;
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                 5; DB 1; L
3.3.8e+05;
1tches 1;
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Pred. No. 3
1; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 10016
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISC
COMPUTER: COMPAQ - IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS VERBION 6.2
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,472C
FILING DATE: 6-JUNE-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/742,908
FILING DATE: 9-AUGUST-1991
APPLICATION NUMBER: US 08/021,606
FILING DATE: 28-JANUARY-1993
ATTORNEY/AGENT INFORMATION:
NAME: ROBINSON, WILLIAM R.
REGISTRATION NUMBER: 27,224
REFERENCE/DOCKET NUMBER: LKR-9122B
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (212) 697-3355
TELEFRAX: NONE
APPLICATION NUMBER: US 08/271,386
FILING DATE: 06-JUL-1994
APPLICATION NUMBER: 08/026,341
FILING DATE: March 4, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Sundsmo, John, S.
REGISTRATION NUMBER: 34,446
REFERENCE/DOCKET NUMBER: 15548-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 1-206-889-5804(direct)
TELEFAX: 1-206-822-3644
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ilarity 60.0%;
Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: AMINO
                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
US-08-415-099A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AMINO ACID
GY: LINEAR
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Best Local Similarity
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2 WIWIW 6
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US-08-467-472C-5
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IDENTIFICATION METHOD: amino acid analysis
IDENTIFICATION METHOD: and
IDENTIFICATION METHOD: mass spectrometry
OTHER INFORMATION: water is removed and
OTHER INFORMATION: thereby
OTHER INFORMATION: a -S- bridge is present between Cys and
PUBLICATION INFORMATION:
AUTHORS: JUNG, GUNTHER
TITLE: PEPTIDES WITH SULFIDE BRIDGES AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19104
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                                                                                                APPLICANT: GOODMAN, MURRAY TITLE OF INVENTION: LANTHIONINE BRIDGED PEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE: N/A
FRAGMENT TYPE: INTERNAL
ORIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE
ORIGINAL SOURCE: INC.,
ORIGINAL SOURCE: 3700 MARKET STREET, PHILADELPHI
IMMEDIATE SOURCE: SYNTHESIZED PEPTIDE
POSITION IN GENOME: N/A
                                                                                                                       NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROOKS HAIDT HAFFNER & DELAHUNTY
STREET: 99 PARK AVENUE
CITY: NEW YORK
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S: JUNG, GUNTHER
PEPTIDES WITH SULFIDE BRIDGES AND
L: PROCEEDINGS OF THE 11TH AMERICAN
L: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07/742,908
FILING DATE: 9-AUGUST-1991
APPLICATION NUMBER: US 08/021,606
FILING DATE: 28-JANUARY-1993
ATTORNEY/AGENT INFORMATION:
NAME: ROBINSON, WILLLIAM R.
REGISTRATION NUMBER: 27,224
REFERENCE/DOCKET NUMBER: LKR-9122B
TELEPHONE: (212) 697-3355
TELEFAX: (212) 557-5635
TELEX: NONE
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                               ZIP: 10016

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" FLOPPY DISC
COMPUTER: COMPAQ - IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS Version 6.2
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,472C
FILING DATE: 6-JUNE-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                  Sequence 6, Application US/08467472C
Patent No. 6028168
GENERAL INFORMATION:
APPLICANT: GOODMAN, MURRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SYMPOSIUM
ESCOM (LEIDEN 1990)
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N/A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE:
DESCRIPTION: PEPT]
HYPOTHETICAL: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                     USA
RESULT 13
US-08-467-472C-6
                                                                                                                                                                                                                                                                COUNTRY:
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Sequence 1500, Application US/09082279B

Patent No. 6258782

GENERAL INFORMATION:

APPLICANT: Barney, Shawn

APPLICANT: Guthrie, Kelly

APPLICANT: Anwer, Mohmed

APPLICANT: Anwer, Mohmed

APPLICANT: Anwer, Mohmed

TITLE OF INVENTION: HYBRID FOLYPEPTIDES WITH ENHANCED

TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES

FILE REFERENCE: 7872-043

CURRENT APPLICATION NUMBER: US/09/082,279B

CURRENT FILING DATE: 1998-05-20

NUMBER OF SEQ ID NOS: 1515

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 8

TYPE: PRT
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Pred. No. 3.8e+05;
1; Mismatches 1;
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Pred. No. 3.8e+05;
l; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                       6: CYS-SER
STRUCTURE
              CYS-SER
                                                                                                                                                                                 CYS-SER
                                                                                                                                                                                                                                                                               11TH AMERICAN
           RELEVANT RESIDUES IN SEQ ID NO: 6: CYS-SPUBLICATION INFORMATION:
AUTHORS: SHIBA, TETSUO
TITLE: CHEMISTRY OF LANTHIONINE PEPTIDES
JOURNAL: BIOPOLYMERS
                                                                                                                                                                                                                         THIOETHER
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                                                                             SUPPLEMENTARY
511 - 519
1986
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                                                                                                                                                                                 SEQ ID NO:
                                                                                                                                                                                                                                                                              PROCEEDINGS OF THE PEPTIDE SYMPOSIUM ESCOM (LEIDEN 1990)
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                                                                                                                                   DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID
PUBLICATION INFORMATION:
AUTHORS: BEAN, MARK F.
TITLE: IDENTIFICATION OF A
TITLE: BY-PRODUCT
TITLE: IN THE SYNTHESIS OF
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nilarity 50.0%;
Conservative
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IN SEQ
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; PUBLICATION DATE:
; RELEVANT RESIDUES I
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US-08-467-472C-6
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Best Local Similarity
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DATE:
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US-09-082-279B-1500
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PUBLICATION
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JOURNAL:
VOLUME:
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DATE:
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FRAGMENT TYPE: INTERNAL
ORIGINAL SOURCE: AMINO ACIDS LISTED IN SE
ORIGINAL SOURCE: INC.,
IMMEDIATE SOURCE: SYNTHESIZED PEPTIDE
POSITION IN GENOME: N/A
FEATURE:
                                                                                             BRIDGED
                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/467,472
FILING DATE:
APPLICATION NUMBER: US 08/021,606
FILING DATE: 28-JANUARY-1993
ATTORNEY/AGENT INFORMATION:
NAME: ROBINSON, WILLIAM R.
REGISTRATION NUMBER: 27,224
REFERENCE/DOCKET NUMBER: LKR-9122B
TELEPHONE: (212) 697-3355
TELEFAX: (212) 557-5635
TELEX: NONE
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                         6.2
US-09-384-061-5

Sequence 5, Application US/09384061

Patent No. 6268339

GENERAL INFORMATION:

TITLE OF INVENTION:

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROOKS HAIDT HAFFNER &

STREET: 99 PARK AVENUE

CITY: NEW YORK

STATE: NY
                                                                                                                                                                                                                             ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISC
COMPUTER: COMPAQ - IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS Version
                                                                                                                                                                                                                                                                                                                     SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/384,061
FILING DATE:
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IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
OTHER INFORMATION: wate
OTHER INFORMATION: a -S
PUBLICATION INFORMATION:
AUTHORS: JUNG, GUNTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GUNTHER
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GY: LINEAR
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DESCRIPTION:
HYPOTHETICAL: N
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PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 5: CYS-SER
PUBLICATION INFORMATION:
AUTHORS: SHIBA, TETSUO
TITLE: CHEMISTRY OF LANTHIONINE PEPTIDES
JOURNE: JOHN WILEY AND SONS, INC.
ISSUE: SUPPLEMENTARY
PAGES: 511 - 519
DATE: 1986
DOCUMENT NUMBER:
FILING DATE:
RELEVANT RESIDUES IN SEQ ID NO: 5: CYS-SER
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 5: CYS-SER
PUBLICATION INFORMATION:
AUTHORS: BEAN, MARK F.
TITLE: IN THE SYNTHESIS OF A CYCLIC DISULFID
TITLE: BY-PRODUCT
TITLE: BY-PRODUCT
TITLE: BY-PRODUCT
TITLE: TANDEM MASS SPECTROMETRY
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
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ed. No. 3.8e+05;
Mismatches 2
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STRUCTURE
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Pred. No.
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Matches 3; Conservative
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summaries

Database

Published

Published Applications AA:*

cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*

cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*

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SUMMARIES

	- 		68,	Sequence 1650, Ap	(")	Sequence 3, Appli	.,	a)		Sequence 38, Appl	Sequence 227, App			
	ID	US-10-046-922-67	US-10-046-922-68	US-10-351-641-1650	US-09-884-767A-38	-452A-	0	US-10-351-641-1655	US-10-196-937A-9	US-10-457-780-38	US-10-367-580-227	US-10-367-593-227	US-10-367-594-227	US-10-367-654-227
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227 227 227 3 1 1 65 87 87 85 87	1180 1180 1180 1180 1133 153 153 153 153 153 153 153 153 15	331 332 332 335 335 336 336 360 360 360 360	525 525 525 525 534 53 53 53 53 53 53 54 53
US-10-367-658- US-10-367-668- US-10-367-674- US-09-155-106- US-10-190-082- US-10-190-082- US-10-858-271-	S-10-190-082 S-10-190-082 S-10-050-902 S-10-050-898 S-10-050-898 S-10-082-014 S-10-149-138	-10-149-13 -10-617-87 -10-617-87 -10-149-13 -10-677-07 -10-477-30 09-947-925	S-10-436-549 S-10-436-549 S-10-712-425 S-10-712-425 S-10-414-524 S-10-346-737 S-09-563-222
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ALIGNMENTS

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                               Sequence 67, Application US/10046922
; Sequence 67, Application US/10046922
; Publication No. US20020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
APPLICANT: Kubo, Hajime
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
; FILE REFERENCE: 28967/37084A
; CURRENT APPLICATION NUMBER: US/10/046,922
; CURRENT APPLICATION NUMBER: US/10/046,922
; CURRENT APPLICATION NUMBER: Datentin version 3.0
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 67
; TYPE: PRT
; ORGANISM: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                         ) NAME/KEY: SITE

) LOCATION: (4)..(6)

) OTHER INFORMATION: X at position 4-6 is any amino acid

US-10-046-922-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 33; DB 13;
Pred. No. 1.5e+06;
; Mismatches
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4; Conservative
RESULT 1
US-10-046-922-67
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Best Local S
Matches 4
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RESULT 2 US-10-046-922-68 ; Sequence 68, Application US/10046922 GYWLTIW GYWXXXW d d ઠે

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OTHER INFORMATION: FC FEATURE:
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ORGANISM: Artificial
FEATURE:
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OTHER INFORMATION: OTHER INFORMATION: 1
FEATURE:
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Matches 3, Conser
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US-10-433-452A-3
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APPLICANT: Anwer, M.
APPLICANT: Anwer, M.
APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: PROPERTIES
FILE REFERENCE: 7872-100
CURRENT APPLICATION NUMBER: US/10/351,641
CURRENT FILING DATE: 2003-01-24
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-05-20
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1757
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1650
LENGTH: 8
LENGTH: 8
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                                                                          INHIBITOR MATERIALS AND METHODS
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Pred. No. 1.5e+06;
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Pred. No. 1.5e+06
); Mismatches
      GENERAL INFORMATION:

APPLICANT: Alitalo, Kari
APPLICANT: Kubo, Hajime
TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERI
FILE REFERENCE: 28967/37084A
CURRENT APPLICATION NUMBER: US/10/046,922
CURRENT FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin version 3.0
SEQ ID NO 68
LENGTH: 8
                                                                                                                                                                                                 TYPE: PRT
ORGANISM: peptide
FEATURE:
NAME/KEY: SITE
LOCATION: (4)..(6)
OTHER INFORMATION: X is any amino acid
NAME/KEY: SITE
LOCATION: (8)..(8)
OTHER INFORMATION: X is any amino acid
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ilarity 57.1%;
Conservative (
Publication No. US20020164667A1
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Merutka, G.
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Matches 4; Conser
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US-10-351-641-1650
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Best Local
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Sequence 38, Application US/09884767A;
Publication No. US20020192789A1
GENERAL INFORMATION:
APPLICANT: DYAX Corp.
APPLICANT: Ley, Arthur C.
APPLICANT: Ladner, Robert C
TITLE OF INVENTION: NOVEL ENTEROKINASE CLEAVAGE SEQUENCES
FILE REFERENCE: DXX-012.1 US, DXX-012.1 PCT
CURRENT APPLICATION NUMBER: US/09/884,767A
CURRENT FILING DATE: 2001-06-19
PRIOR PPLICATION NUMBER: US 09/597,321
PRIOR FILING DATE: 2000-06-19
NUMBER OF SEQ ID NOS: 217
SOFTWARE: PatentIn version 3.1
SEQ ID NO 38
LENGTH: 7
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Pred. No. 1.5e+06;
); Mismatches 3;
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Pred. No. 1.5e+06;
1; Mismatches 0
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OTHER INFORMATION: Xaa is a less conserved or
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Sequence 3, Application US/10433452A;
Publication No. US20040101905A1
GENERAL INFORMATION:
APPLICANT: Brekke, Ole Henrik
APPLICANT: Lauvrak, Vigdis
APPLICANT: Sandlie, Inger
TITLE OF INVENTION: Hybrid Antibodies
FILE REFERENCE: DEH-0014
CURRENT APPLICATION NUMBER: US/10/433,452A
CURRENT FILING DATE: 2003-11-24
PRIOR FILING DATE: 2000-12-01
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patentin version 3.2
SEQ ID NO 3
LENGTH: 7
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F, tyrosine:
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ORGANISM: Artificial Sequence
FEATURE:
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ilarity 75.0%;
Conservative
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nilarity 50.0%;
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RESULT 4 US-09-884-767A-38

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Sequence 1655, Application US/10351641

Publication No. US20030186874A1

GENERAL INFORMATION:

APPLICANT: Barney, S.

APPLICANT: Anwer, M.

APPLICANT: Anwer, M.

APPLICANT: Lambert, D.

TITLE OF INVENTION: PROPERTIES

FILE REFERENCE: 7872-100

CURRENT APPLICATION NUMBER: US/10/351,641

FRIOR APPLICATION NUMBER: 09/350,641

PRIOR FILING DATE: 1999-07-09

PRIOR FILING DATE: 1999-07-09

PRIOR FILING DATE: 1999-05-20

PRIOR FILING DATE: 1999-05-20

PRIOR FILING DATE: 1999-05-20

PRIOR FILING DATE: 1999-05-30

PRIOR FILING DATE: 1998-05-20

WUMBER OF SEQ ID NOS: 1757

SOFTWARE: FRELSEQ for Windows Version 3.0

SEQ ID NO 1655
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Pred. No. 1.5e+06;
                         Sequence 5, Application US/09852870A; Sequence 5, Application US/09852870A; Patent No. US20020165132A1; GENERAL INFORMATION:
APPLICANT: Goodman, Murray, APPLICANT: Osapay, George; TITLE OF INVENTION: Lanthionin Bridged Proteins; FILE REFERENCE: LKR 9122-D; CURRENT APPLICATION NUMBER: US/09/852,870A; CURRENT FILING DATE: 2001-05-10; PRIOR APPLICATION NUMBER: US 09/384,601; PRIOR FILING DATE: 1999-08-26; NUMBER OF SEQ ID NOS: 24; SOFTWARE: Patentin version 3.0; SEQ ID NO 5; LENGTH: 8
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Pred. No. 1.5e+06;
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illarity 60.0%;
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ORGANISM: Artificial Sequence
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US-10-351-641-1655
RESULT 6
US-09-852-870A-5
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US-10-196-937A-9
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RESULT 9
US-10-457-780-38
; Sequence 38, Application US/10457780
; Publication No. US20040137426A1
; GENERAL INFORMATION:
; APPLICANT: SERRES, Joseph
; TITLE OF INVENTION: TO TARGET CELLS
; FILE REFERENCE: 118761
; CURRENT APPLICATION NUMBER: US/10/457,780
; CURRENT PILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: US 60/446,268
; PRIOR PILING DATE: 2003-02-11
; PRIOR PILING DATE: 2003-02-11
; PRIOR PILING DATE: 2002-09-27
; PRIOR PILING DATE: 2002-06-10
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Sequence 9, Application US/10196937A;
Publication No. US20040024176A1;
GENERAL INFORMATION:
APPLICANT: Ghadiri, Reza M.
TITLE OF INVENTION: Cyclic Peptide Tube;
FILE REFERENCE: 397.2 Div 1/SCR 2381;
CURRENT APPLICATION NUMBER: US/10/196,937A;
PRIOR APPLICATION NUMBER: 08/632,444
PRIOR APPLICATION NUMBER: 08/632,444
PRIOR FILING DATE: 1996-04-15;
PRIOR FILING DATE: 1994-10-11
PRIOR APPLICATION NUMBER: 08/138,502
PRIOR FILING DATE: 1993-10-14
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
LENGTH: 8
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Local Similarity 60.0%;
hes 3; Conservative
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ORGANISM: Artificial
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LOCATION: 8
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APPLICANT: Houghton, Alan
APPLICANT: Takechi, Yoshizumi
APPLICANT: Takechi, Yoshizumi
APPLICANT: Mayhew, Mark
TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
FILE REFERENCE: 11746/461012
CURRENT APPLICATION NUMBER: US/10/367,593
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                                                                                                            Score 26; DB 16; 1
Pred. No. 1.5e+06;
; Mismatches 1;
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Pred. No. 1.5e+06;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                            Sequence 227, Application US/10367580

Sequence 227, Application US/10367580

Publication No. US20040071720A1

GENERAL INFORMATION:
APPLICANT: Rothman, James E.
APPLICANT: Harth, F. Ulrich
APPLICANT: Houghton, Alan
APPLICANT: Takechi, Yoshizumi
APPLICANT: Aayhew, Mark
TITLE OF INVENTION: Heat Shock Protein-Based
FILE REFERENCE: 11746/461061
CURRENT APPLICATION NUMBER: US/10/367,580
CURRENT FILING DATE: 2003-02-14
PRIOR FILING DATE: 2001-02-27
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1996-08-16
PRIOR FILING DATE: 1996-08-16
PRIOR FILING DATE: 1995-08-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: synthetic peptide S-10-367-580-227
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Publication No. US20040071721A1
GENERAL INFORMATION:
APPLICANT: Rothman, James E.
APPLICANT: Hartl, F. Ulrich
APPLICANT: Hoe, Mee H.
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                                                                                                                               Similarity 60.3; Conservative
; TYPE: PRT
; ORGANISM: Artificial Seq;
; FEATURE:
; OTHER INFORMATION: r-W8F
US-10-457-780-38
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US-10-367-580-227
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APPLICANT: Rothman, James E.
APPLICANT: Hartl, F. Ulrich
APPLICANT: Houghton, Alan
APPLICANT: Houghton, Alan
APPLICANT: Houghton, Alan
APPLICANT: Takechi, Yoshizumi
APPLICANT: Mayhew, Mark
TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
FILE REFERENCE: 11746/461041
CURRENT APPLICATION NUMBER: US/10/367,594
CURRENT FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: US 09/680,806
PRIOR PILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1996-08-16
PRIOR APPLICATION NUMBER: US 60/002,490
PRIOR APPLICATION NUMBER: US 60/002,479
PRIOR APPLICATION NUMBER: US 60/002,479
PRIOR FILING DATE: 1995-08-18
PRIOR FILING DATE: 1995-08-18
PRIOR FILING DATE: 1995-08-18
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1.5e+06;
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Pred. No. 1.5e+06;
; Mismatches 0;
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Pred. No. 1.5e
2; Mismatches
CURRENT FILING DATE: 2003-02-14
PRIOR APPLICATION NUMBER: US 09/011,645
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1996-08-16
PRIOR FILING DATE: 1996-08-16
PRIOR FILING DATE: 1995-08-18
PRIOR FILING DATE: 1995-08-18
PRIOR FILING DATE: 1995-08-18
PRIOR FILING DATE: 1995-08-18
NUMBER OF SEQ ID NOS: 349
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 227
LENGTH: 8
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SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 227
LENGTH: 8
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                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: synthetic peptide US-10-367-593-227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 227, Application US/10367594
Publication No. US20040071722A1
GENERAL INFORMATION:
APPLICANT: Rothman, James E.
APPLICANT: Hartl, F. Ulrich
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Best Local Similarity 57.1%;
Matches 4; Conservative
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Best Local Similarity
Matches 4; Conser
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APPLICANT: Rothman, James E.
APPLICANT: Hartl, F. Ulrich
APPLICANT: Hoe, Mee H.
APPLICANT: Houghton, Alan
APPLICANT: Takechi, Yoshizumi
APPLICANT: Takechi, Yoshizumi
APPLICANT: Takechi, Yoshizumi
APPLICANT: Takechi, Yoshizumi
APPLICANT: Mayhew, Mark
TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and
FILE REFERENCE: 1746/461051
CURRENT APPLICATION NUMBER: US 09/794,529
PRIOR PILING DATE: 2001-02-27
PRIOR PILING DATE: 1998-02-13
PRIOR FILING DATE: 1996-08-16
PRIOR FILING DATE: 1996-08-16
PRIOR FILING DATE: 1995-08-18
PRIOR FILING DATE: 1995-08-18
NUMBER OF SEQ ID NOS: 349
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 25.5; DB 15;
Pred. No. 1.5e+06;
2; Mismatches 0;
                                                                                                                         APPLICANT: Hartl, F. Ulrich
APPLICANT: Hoe, Mee H.
APPLICANT: Houghton, Alan
APPLICANT: Houghton, Alan
APPLICANT: Takechi, Yoshizumi
APPLICANT: Takechi, Yoshizumi
APPLICANT: Mayhew, Mark
TITLE OF INVENTION: Heat Shock Protein-Based
FILE REFERENCE: 11746/461032
CURRENT APPLICATION NUMBER: US/10/367,654
CURRENT FILING DATE: 2003-02-14
PRIOR FILING DATE: 2000-06-13
PRIOR FILING DATE: 2000-08-10
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1996-08-16
PRIOR FILING DATE: 1996-08-16
PRIOR FILING DATE: 1996-08-16
PRIOR FILING DATE: 1996-08-18
PRIOR FILING DATE: 1995-08-18
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SOFTWARE: WordPerfect 8.0 for Windows
EQ ID NO 227
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                       Application US/10367654 o. US20040071723A1
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ORGANISM: Artificial Sequence
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Best Local Similarity 57.1%;
Matches 4; Conservative
                                                                                   APPLICANT: Rothman, James E. APPLICANT: Hartl, F. Ulrich APPLICANT: Hoe, Mee H. APPLICANT: Houghton, Alan APPLICANT: Takechi, Yoshizur
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US-10-367-654-227
; Sequence 227, Application No. US201; GENERAL INFORMATION:
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APPLICANT: Rothman, James E.
APPLICANT: Hartl, F. Ulrich
APPLICANT: Hoe, Mee H.
APPLICANT: Hoe, Mee H.
APPLICANT: Houghton, Alan
APPLICANT: Takechi, Yoshizumi
APPLICANT: Mayhew, Mark
TITLE OF INVENTION: Haat Shock Protein-Based Vaccines and Immu
FILE REFERENCE: 11746/461072
CURRENT APPLICATION NUMBER: US 09/794,517
PRIOR PILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: US 09/011,645
PRIOR FILING DATE: 1996-08-16
PRIOR FILING DATE: 1996-08-16
PRIOR FILING DATE: 1995-08-18
PRIOR FILING DATE: 1995-08-18
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NUMBER OF SEQ ID NOS: 349
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Pred. No. 1.5e+06;
2; Mismatches 0;
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Pred. No. 1.5e+06;
2; Mismatches 0;
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               TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic peptide
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                                                                                                                                                                                                                                                                                                                                 Sequence 227, Application US/10367668 Publication No. US20040071725A1 GENERAL INFORMATION: APPLICANT: Rothman, James E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2;
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Similarity 57.1%;
4; Conservative 2
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larity 57.1%;
Conservative
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Best Local Similarity
Matches 4; Conser
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1 GWWVT-W
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1 GWWVT-W
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US-10-367-668-227
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5.1.6 Compugen Ltd version : - 2005 (GenCore (c) 1993 Copyright

model **₹** using protein search, OM protein

; Search time 38 Seconds (without alignments) 20.256 Million cell update 12:22:35 2005, 3, January Run on:

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SEQ32 54

BCore Title: Perfect

gywltiwg Sequence:

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BLOSUM62 Scoring table

Gapext 0.5 -Gapop 10.0

Searched:

of hits satisfying chosen parameters: 283416 seqs, Total number

residues

96216763

909

Minimum DB seq length: 0 MaximumWDBmseqWlength: 1863

Post-processing: Minimum Match Maximum Match Listing first

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PIR Database

R 79: *
Dir1: *
Dir2: *
Dir3: * H 0 6 4

ve a printed, Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being pand is derived by analysis of the total score distribution.

	Description	T-cell receptor be	pentapeptide	Jeucokinin V - Mad	e11	ell	ell receptor	пв	ell receptor	ell re	ell receptor	ell receptor b	curonosyltran	at	1 - pe						eucokinir		okinin VI	otensin	hypothetical prote	ll recept	급	irotoxin - dest	H 6	Vesicle associated
SUMMARIES	Ω	PT0586	025	JS0315	328	062	063	106	062	064	072	072	000	839	002	727	324	324	324	072	031	031	031	157	965	053	194	872	H161	4
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ALIGNMENTS

T-cell receptor beta chain V-D-J region (141-1CN) - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C; Accession: PT0586; PT0592
R; Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A; Title: Junctional sequences of fetal T cell receptor beta chains have few N regions. A; Reference number: PT0509; MUID:91277601; PMID:1711558
A; Reference number: PT0586
A; Reference number: PT0586
A; Residues: translation not shown
A; Molecule type: mRNA
A; Residues: 1-7 < FEE>
A; Residues: 1-7 < FEE>
A; Experimental source: day 19 fetal thymus, strain BALB/c (clones 141-1CN and 141-1CD)
C; Keywords: T-cell receptor

ö Gapa ö 7; IndelB Length DB 2; Ler 2.8e+05; Mismatches Score 22; Pred. No. 40.7%; illarity 75.0%; Conservative Similarity 3; Conserv Query Match Best Local S Matches 3

æ 9 SIWG 5 TIWG g ਨੇ

RESULT 2 JH0253

eel

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esophagogastr gut pentapeptide - Japanese eel
C;Species: Anguilla japonica (Japanese eel)
C;Species: Anguilla japonica (Japanese eel)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 11-Apr-1995
C;Accession: JH0253
R;Uesaka, T.; Ikeda, T.; Kubota, I.; Muneoka, Y.; Ando, M.
Biochem. Biophys. Res. Commun. 180, 828-832, 1991
A;Title: Structure and function of a pentapeptide isolated from the gut of A;Reference number: JH0253; MUID:92062113; PMID:1953755
A;Accession: JH0253
A;Molecule type: protein
A;Residues: 1-5 <UES>
A;Experimental source: gut
C;Comment: This peptide increased basal tone of the circular muscle of the c;comment: and of the circular muscle of the gastro-intestinal junction.

.. 0 Indela Length 5; Score 20; DB 2; L6 Pred. No. 2.8e+05; 1; Mismatches 0; 37.0%; larity 66.7%; Conservative 1 Query Match Best Local Similarity Matches 2; Conser

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T cell receptor beta chains have few N regions.
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A61068
locustakinin - migratory locust
C; Species: Locusta migratoria (migratory locust)
C; Species: Locusta migratoria (migratory locust)
C; Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C; Accession: A61068
R; Schoofs, L.; Holman, G.M.; Proost, P.; Van Damme, J.; Hayes, T.K.; De Loof, Regul. Pept. 37, 49-57, 1992
A; Title: Locustakinin, a novel myotropic peptide from Locusta migratoria, isol A; Title: Locustakinin, a novel myotropic peptide from Locusta migratoria, isol A; Residues: A61068, MUID:92262851; PMID:1585017
A; Residues: 1-6 <SCH>
A; Cross-references: UNIPROT:P41491
C; Keywords: amidated carboxyl end; cephalomyotropic peptide; neuropeptide F; 6/Modified site: amidated carboxyl end (Gly) #status experimental
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PT0637
T-cell receptor beta chain V-D-J region (111-1K) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0637
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0637
A;Accession: PT0637
A;Accession: translation not shown
A;Molecule type: mRNA
A;Esidues: 1-6 <FEE>
A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell receptor
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PT0628
T-cell receptor beta chain V-D-J region (111-1AG) -
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992
C;Accession: PT0628
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell recep
  BALB/c,
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                                                                Score 17;
Pred. No.
A; Experimental source: adult thymus, strain C; Keywords: T-cell receptor
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2; Conservative
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1
C;Accession: B53284
R;Harindranath, N.; Alexander, C.B.; Mage, R.G.
Mol. Immunol. 28, 881-888, 1991
A;Title: Evolutionarily conserved organization and sequences of germline
A;Reference number: A53284; MUID:91342695; PMID:1678859
A;Accession: B53284
A;Accession: B53284
A;Accession: B53284
A;Accession: B53284
A;Accession: B53284
A;Accession: B53284
A;Cross-references: GB:S60737; NID:g233916; PIDN:AAB19518.1; PID:g233918
A;Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBIP:60738)
C;Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 have
                                                           C; Species: Leucophaea maderae (Madeira cockroach)
C; Species: Leucophaea maderae (Madeira cockroach)
C; Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-C; Accession: JS0315
R; Holman, G.M.; Cook, B.J.; Nachman, R.J.
Comp. Biochem. Physiol. C 88, 27-30, 1987
A; Title: Isolation, primary structure, and synthesis of leucokinins V a A; Reference number: JS0315
A; Reference number: JS0315
A; Molecule type: protein
A; Molecule type: protein
A; Residues: 1-8 < HOL>
A; Residues: 1-8 < HOL>
C; Comment: Leucokinins, a family of cephalomyotropic peptide
C; Keywords: amidated carboxyl end; cephalomyotropic peptide
F; 8/Modified site: amidated carboxyl end (Gly) #status experimental
                                                                                         09-J
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C; Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-1
C; Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-1
C; Accession: PT0629; PT0528
A; Reference number: PT0509; MUID:91277601; PMID:1711558
A; Reference number: PT0509; MUID:91277601; PMID:1711558
A; Residues: translation not shown
A; Molecule type: mRNA
A; Residues: 1-6 < FEE>
A; Experimental source: newborn thymus, strain BALB/C, clone 100-2AH
A; Accession: PT0528
A; Status: translation not shown
A; Molecule type: mRNA
A; Residues: 1-6 < FEE>
A; Residues: 1-6 < FEE>
A; Residues: 1-6 < FEE>
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Pred. No. 2.8e+05;
1; Mismatches 4;
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Best Local Similarity 37.5%;
Matches 3; Conservative
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glucuronosyltransferase (EC 2.4.1.17), hepatic - rat (fragment)

Sjucuronosyltransferase (EC 2.4.1.17), hepatic - rat (fragment)

N;Alternate names: UDP-glucuronyltransferase
C;Species: Rattus norvegicus (Norway rat)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 07-Feb-1997
C;Accession: PX0008
R;Yokota, H.; Yuasa, A.; Sato, R.
J. Biochem. 104, 531-536, 1988
A;Title: Purification and properties of a form of UDP-glucuronyltransferase
A;Reference number: PX0008; MUID: 89197852; PMID: 3149280
A;Reference number: PX0008
A;Accession: PX0008
A;Molecule type: protein
A;Residues: 1-7 <YOK>
C;Keywords: glycosyltransferase; hexosyltransferase; liver
            30-May-1997
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   C; Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change C; Accession: PT0728
R; Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A; Title: Junctional sequences of fetal T cell receptor beta chai A; Reference number: PT0509; MUID: 91277601; PMID:1711558
A; Accession: PT0728
A; Accession: PT0728
A; Status: translation not shown
A; Molecule type: DNA
A; Residues: 1-7 < FEE>
A; Experimental source: newborn thymus, strain BALB/c
C; Keywords: T-cell receptor
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C; Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change C; Accession: B48394
R; Mather, I.H.; Banghart, L.R.; Lane, W.S.
Biochem. Mol. Biol. Int. 29, 545-554, 1993
A; Title: The major fat-globule membrane proteins, bovine componi II-like sequences.
A; Reference number: A48394; MUID:93250576; PMID:8485470
A; Accession: B48394
A; Status: preliminary
A; Molecule type: protein
A; Residues: 1-7 < MAT>
A; Residues: 1-7 < MAT>
A; Note: sequence extracted from NCBI backbone (NCBIP:131444)
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C; Species: Mus musculus (house mouse)
C; Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-NC; Accession: PT0722
R; Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A; Title: Junctional sequences of fetal T cell receptor beta chains PA; Reference number: PT0509; MUID:91277601; PMID:1711558
A; Reference number: PT0509; MUID:91277601; PMID:1711558
A; Reference number: PT0722
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-7 < FEE>
A; Experimental source: newborn thymus, strain BALB/C
C; Keywords: T-cell receptor
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C; Species: Mus musculus (house mouse)
C; Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-1
C; Accession: PT0642
R; Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A; Title: Junctional sequences of fetal T cell receptor beta chains A; Reference number: PT0509; MUID: 91277601; PMID: 1711558
A; Accession: PT0642
A; Status: translation not shown
A; Molecule type: mRNA
A; Residues: 1-7 < FEE>
A; Experimental source: newborn thymus, strain BALB/C
C; Keywords: T-cell receptor
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0; Mismatches 0;
A; Reference number: PT0509; MUID:91277601; PMID:171
A; Accession: PT0628
A; Status: translation not shown
A; Molecule type: mRNA
A; Residues: 1-7 < FEE>
A; Experimental source: newborn thymus, strain BALB/
C; Keywords: T-cell receptor
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S57274
triacylglycerol lipase (EC 3.1.1.3) - Psychrobacter immobilis (fragment)
C; Species: Psychrobacter immobilis
C; Species: Psychrobacter immobilis
C; Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2
C; Accession: S57274
R; Arpigny, J.L.; Feller, G.; Gerday, C.
Biochim. Biophys. Acta 1263, 103, 1995
A; Title: Corrigendum to "Cloning, sequence and structural features of a A; Reference number: S57274; MUID:95359197; PMID:7632728
A; Accession: S57274
A; Accession: S57274
A; Molecule type: DNA
A; Residues: 1-7 < ARP>
A; Residues: 1-7 < ARP>
C; Keywords: carboxylic ester hydrolase
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pev-kinin 1 - penaeid shrimp (Penaeus vannamei) (fragment)
C;Species: Penaeus vannamei
C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 19-Mac;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 19-Mac; Accession: PD0029
R;Nieto, J.; Veelaert, D.; Derua, R.; Waelkens, E.; Cerstiaens, A.; (Biochem. Biophys. Res. Commun. 248, 406-411, 1998
A;Title: Identification of one tachykinin- and two kinin-related pepth A;Reference number: PD0027; MUID: 98342103; PMID: 9675150
A;Reference type: protein
A;Residues: 1-7 <NIE>
C;Comment: This peptide belongs to myotropic neuropeptides.
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Matches 2; Conservative 0; Mismatches 0;
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Matches 2; Conservative 0; Mismatches 0;
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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd Copyright

using sw model - protein search, OM protein

2005, 12:14:40 a, January Run on:

updates/sec ; Search time 189 Seconds (without alignments) 24.354 Million cell update

gywltiwg SEQ32 54 1 gyw] score: Sequence: Title: Perfect

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Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1825181 segs, 575374646 residues Searched:

835 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

UniProt_02:*
1: uniprot_grot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		d			SUMMAKIES	
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ALIGNMENTS

RESULT Q70Y57	57			
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F4	5-JUL-20	27,	Last annot	annotation update)
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z	ame=rps1			
တ	Fuerstia afri	icana.		-
ō	Chloroplast.			
ပ္ပ	Eukaryota; Viri	iridiplantae; St	reptophyta	Embryophyta; Tracheophyta;
	Spermatophyt	a; Magnoliophyta	; endicoty	•
	lamiids; Lam	iales; Lamiaceae;	; Nepetoid	Nepetoideae; Ocimeae; Fuerstia.
	NCBI_TaxID=20422	04226;		
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	SEQUENCE FRO	M N.A.		
	PubMed=15019	625;		
	Paton A., Sp	ringate D.A., Su	idde S., Ot:	Sudde S., Otieno D., Grayer R., Harley M.M.,
	Willis F., S	imonds M.S.J., P	owell M.P.	Savolainen V.;
	"Phylogeny a	nd evolution of	basils and	allies (Ocimeae, Labiatae)
	based on thr	ee plastid DNA r	egions.";	
	Mol. Phylogenet.	Mol. Phylogenet. Evol. 31:277-299(2004)	7-299 (2004)	-
	EMBL; AJ5054	27; CAD45547.1;	;	
DR	GO; GO: 00037	35; F:structural constituent	constitue	it of ribosome; IEA.
	Ribosomal pr	otein.		
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DT 14-MAR-2004 (TrEMBLrel. 27, Created)

DT 14-MAR-2004 (TrEMBLrel. 27, Last sequence update)

DT 14-MAR-2004 (TrEMBLrel. 27, Last annotation update)

DT 14-MAR-2004 (TrEMBLrel. 27, Last annotation update)

DT 14-MAR-2004 (TrEMBLrel. 27, Last annotation update)

DF Ribosomal protein (Fragment).

GN RPS16.

OS Fuerstia africana.

OG Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;

OC Spermatophyta; Lamiaceae; Nepetoideae; Ocimeae; Fuerstia.

OX NCBI_TaxID=204226;

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                                     Grayer R., Harley M.M.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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MEDLINE=95156893; PubMed=7853788;
Nakazato H., Hattori S., Ushijima T., Matsuura T., Koitabashi Takada T., Yoshioka K., Endo F., Matsuda I.;
"Mutations in the COL4A5 gene in Alport syndrome: a possible n in primordial germ cells.";
Kidney Int. 46:1307-1314(1994).
EMBL; S75903; AAB33374.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22056123; PubMed=12060770;
Beerenwinkel N., Schmidt B., Walter H., Kaiser R., Lengauer
Hoffmann D., Korn K., Selbig J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                               Paton A., Springate D.A., Sudde S., Otieno D., Grayer R. Willis F., Simonds M.S.J., Powell M.P., Savolainen V.; "Phylogeny and evolution of basils and allies (Ocimeae, based on three plastid DNA regions."; Mol. Phylogenet. Evol. 31:277-299(2004). EMBL; AJ505427; CAD45547.1; -. Chloroplast; Ribosomal protein.
                                                                                                                                                                                                                                               Length
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Viruses, Retroid viruses, Retroviridae, Lentivirus
NCBI TaxID=11676;
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                                                                                                                                                                                                         DABEAB58637041B5 CRC64;
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Pred. No. 1.8e+06;
0; Mismatches 0;
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01-OCT-2002 (TrEMBLrel. 22, Creat
01-OCT-2002 (TrEMBLrel. 22, Last
01-OCT-2002 (TrEMBLrel. 22, Last
Truncated pol protein (Fragment)
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02-MAR-2004 (TrEMBLrel. 27, C
02-MAR-2004 (TrEMBLrel. 27, L
02-MAR-2004 (TrEMBLrel. 27, L
Collagen alpha 5(IV) chain (F
                                                                                                                                                                                                                                            48.1%;
100.0%;
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ilarity 40.0%;
Conservative
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4; Conservative
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SEQUENCE FROM N.A
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Best Local S
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TISSUE=Fibroblast;

X MEDLINE=95009907; PubMed=7523108;

MEDLINE=95009907; PubMed=7523108;

A Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;

T "Separation and sequencing of familiar and novel murine proteins using preparative two-dimensional gel electrophoresis.";

Electrophoresis 15:735-745(1994).

Electrophoresis 15:735-745(1994).

C -1- MISCELLANEOUS: On the 2D-gel the determined pl of this unknown protein is: 6.6, its MW is: 19 kDa.

CC protein is: 6.6, its MW is: 19 kDa.
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 bioinformatics
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TISSUE=Head;
MEDLINE=87052651; PubMed=2877794;
MEDLINE=87052651; PubMed=2877794;
Holman G.M., Cook B.J., Nachman R.J.;
Holman G.M., Cook B.J., Nachman R.J.;
"Isolation, primary structure, and synthesis of leucokinins V and V myotropic peptides of Leucophaea maderae.";
myotropic peptides of Leucophaea maderae.";
Comp. Biochem. Physiol. 88C:27-30(1987).
-!- FUNCTION: This cephalomyotropic peptide stimulates contractile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
NCBI_TaxID=10090;
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Leucokinin V (L-V).
Leucophaea maderae (Madeira cockroach).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea,
Blaberidae; Leucophaea.
NCBI_TaxID=6988;
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  resistance
                                                                                               76C37731A046C700 CRC64;
"Diversity and complexity of HIV-1 drug resistand approach to predicting phenotype from genotype."

Proc. Natl. Acad. Sci. U.S.A. 99:8271-8276(2002)

EMBL; AF347267; AAK32344.1; -.

NON_TER 1
                                                                                                                                  Score 20; DB 2; Lo Pred. No. 1.8e+06; 2; Mismatches 0;
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1.8e+06;
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01-OCT-1994 (Rel. 30, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Unknown protein from 2D-PAGE of fibroblasts (
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05-JUL-2004
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Sciurognathi; Muridae; Murinae; Ra
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-!- MASS SPECTROMETRY: MW=838.15; METHOD=Electrospray; RANGE=1
NOTE=Ref.1.
                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
Blattidae; Periplaneta.
NCBI_TaxID=6978;
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TISSUE=Corpora cardiaca;
MEDLINE=98010462; PubMed=9350979;
Predel R., Kellner R., Rapus J., Penzlin H., Gade G.;
"Isolation and structural elucidation of eight kinins from retrocerebral complex of the American cockroach, Periplane
                                                                                                                      IndelB
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Last annotation update)
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-!- FUNCTION: Mediates visceral muscle contractile
activity).
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                                                  Neuropeptide amide.
                                                                         CRC64
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                                                                                               Score 18; DB 1;
Pred. No. 1.8e+06;
L; Mismatches 4
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Pred. No. 1.8e+06
; Mismatches
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05-JUL-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Kinin-4 (Pea-K-4).
Periplaneta americana (American cockroach).
                protodeum (hindgut)
Secreted.
                                                  sequencing; Neurol
Glycine amide.
736365A5B9C865B8
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STRAIN=Fisher;
MEDLINE=95331633; PubMed=7607556;
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Chordata;
Rodentia;
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ilarity 37.5%;
Conservative
activity of cockroach p
-!- SUBCELLULAR LOCATION: So
PIR; JS0315; JS0315.
Amidation; Direct protein er
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larity 37.5%;
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O62721;
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01-NOV-1996 (TrEMBLrel. C
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Mammalia; Eutheria;
NCBI_TaxID=10116;
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/ be important in the stimulation of diuretic activity in Malpighian
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Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
Sigmurethra; Achatinoidea; Achatinidae; Achatina.
NCBI_TaxID=6530;
                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Locustakinin, a novel myotropic peptide from Locusta migratoria, isolation, primary structure and synthesis.";
Regul. Pept. 37:49-57(1992).
-I- FUNCTION: Myotropic peptide. May be important in the stimulate of ion transport and inhibition of diuretic activity in Malpig
Altus M.S., Wood C.M., Stewart D.A., Roskams A.I., Friedman V., Henderson T., Owens G.A., Danner D.B., Jupe E.R., Dell'Orco R.T
                                      human
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
Acridoidea; Acrididae; Oedipodinae; Locusta.

NCBI_TaxID=7004;
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MEDLINE=92262851; PubMed=1585017;
Schoofs L., Holman G.M., Proost P., van Damme J., Hayes T.K.,
de Loof A.;
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Amidation; Direct protein sequencing; Neuropeptide
MOD RES 6 Glycine amide.
centrence 6 AA; 654 MW; 686365A5B9CDB000 CRC64;
                                    conservation between the
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(Rel. 32, Last sequence update)
(Rel. 44, Last annotation update)
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(Rel. 44, Last annotation update)
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Pred. No.
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                      McClung J.K.;

"Regions of evolutionary conse prohibitin-encoding genes.";
Gene 158:291-294(1995).

EMBL; U17178; AAA86692.1; -.
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ilarity 40.0%;
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01-NOV-1995
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05-JUL-2004
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01-JUN-1994
05-JUL-2004
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TISSUE=Muscle;
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Sigmurethra; Achatinoidea; Achatinidae; Achatina.
NCBI_TaxID=6530;
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MEDLINE=93265912; PubMed=8495720;
Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
Minakata H., -2 and -3: novel neuromodulatory peptides isolated
ganglia of the African giant snail, Achatina fulica.";
FEBS Lett. 323:104-108(1993).
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                 M., Nomoto K.;
peptides isolated
fulica.";
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TISSUE=Ganglion;
MEDLINE=93265912; PubMed=8495720;
Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
"Wwamide-1, -2 and -3: novel neuromodulatory peptides isolat ganglia of the African giant snail, Achatina fulica.";
FEBS Lett. 323:104-108(1993).
-!- FUNCTION: Exhibits modulatory effects on the peripheral
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Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata;
Sigmurethra; Achatinoidea; Achatinidae; Achatina.
NCBI_TaxID=6530;
                                                             system. Inhibits activity on a central neuron. PIR; S33245; S33245. Amidation; Direct protein sequencing; Neuropeptide MOD RES 7 7 Tryptophan amide. SEQUENCE 7 AA; 993 MW; 7362D5B69B041310 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                          Amidation; Direct protein sequencing; Neuropeptide MOD RES 7 7 Tryptophan amide. SEQUENCE 7 AA; 964 MW; 7362D5B686D32310 CRC64;
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Pred. No. 1.8e+06;
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on update)
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01-JUN-1994 (Rel. 29, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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(Rel. 44, Last annotation
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05-JUL-2004
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ACI THUAL STANDARD; FRT; 8 AA.
P18691;
01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 14, Last sequence update)
01-NOV-1990 (Rel. 44, Last annotation update)
Angiotensin-converting enzyme inhibitor.
Thunnus albacares (Yellowfin tuna) (Neothunnus macropterus).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
Scombridae; Thunnus.
NCBI_TaxID=8236;
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049223;
049223;
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-1998 (TrEMBLrel. 19, Last annotation update)
01-JUN-1998 (TrEMBLrel. 19, Last annotation update)
HMG-1-like protein (Fragment).
Glycine max (Soybean).
Glycine max (Soybean).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Roots;
MEDLINE=91367679; PubMed=1891369;
Laux T., Goldberg R.B.;
"A plant DNA binding protein shares highly conserved sequence motifs with HMG-box proteins.";
Nucleic Acids Res. 19:4769-4769(1991).
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  isolated
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fulica.";
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Tryptophan amide.
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snail, Achatina
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"Wwamide-1, -2 and -3: novel not
ganglia of the African giant so
FEBS Lett. 323:104-108(1993).
PIR; S33244; S33244.
Amidation; Direct protein seque
MOD_RES
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100.0%;
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Submitted (FEB-1998) to the
EMBL; AF047050; AAC03556.1;
NON TER
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two neuropeptides from
Cephalomyotropins.";
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MEDLINE=88326322; PubMed=3415688;
Kohama Y., Matsumoto S., Oka H., Teramoto T., Okabe M., Mimura
"Isolation of angiotensin-converting enzyme inhibitor from tuna
muscle.";
                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Leucokinin I (L-I).
Leucophaea maderae (Madeira cockroach).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
Blaberidae; Leucophaea.
NCBI_TaxID=6988;
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TISSUE=Head;
Holman G.M., Cook B.J., Nachman R.J.;
Holman G.M., Cook B.J., Nachman R.J.;
Holman G.M., Cook B.J., Nachman R.J.;
"Isolation, primary structure and synthesis of two neulatoract brochae maderae: members of a new family of Cephalc Comp. Biochem. Physiol. 84C:205-211(1986).

-!- FUNCTION: This cephalomyotropic peptide stimulateractivity of cockroach protodeum (hindgut).

-!- SUBCELLULAR LOCATION: Secreted.
Amidation; Direct protein sequencing; Neuropeptide.
Amidation; Direct protein sequencing; Neuropeptide.
MOD RES
8 8 Glycine amide.
SEQUENCE 8 AA; 893 MW; DC6365B449CDC76A CRC64;
                                                                 Biochem, Biophys. Res. Commun. 155:332-337(1988).
-1- FUNCTION: Inhibits angiotensin-converting enzyme.
PIR; A31570; A31570.
Direct protein sequencing; Metalloprotease inhibitor.
SEQUENCE 8 AA; 953 MW; 6AA863733051F1B7 CRC64;
                                                                                                                                                                        Score 17; DB 1; Le
Pred. No. 1.8e+06;
0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; P
Matches 2; Conservative 0;
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